

From:

Bunner, Bridget

Sent:

Tuesday, August 16, 2005 3:31 PM STIC-Biotech/ChemLib

To: Subject:

sequence search

Hi! I'd like to request the following sequence search for case 09/762,594 (please also include the pending databases):

- 1. the nucleic acid sequence of SEQ ID NO: 2
- 2. the nucleic acid sequence encoding the protein of SEQ ID NO: 7

Thanks!

Bridget Bunner

Art Unit 1647 Rem 4C65 (571) 272-0881 mailbox 4C70

STAFF USE ONLY

Searcher:
Searcher Phone: 2Date Searcher Picked was
Date Completed:

Searcher Prep/Rev. Time:
Online Time:

Type of Search

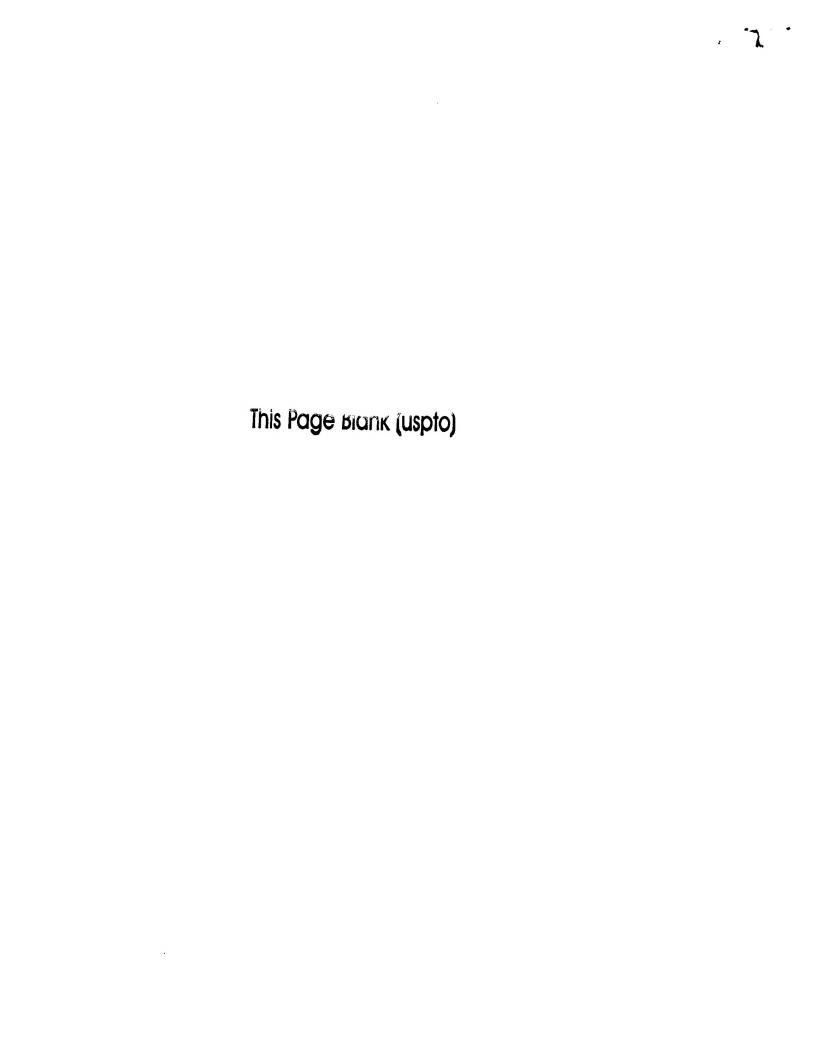
NA#:_____ AA#:___ | ____ Fevels
Interference:____ SPDI:___ FO MA
S/L:_____ Oligomer:___

Encode/Transl:_____ Text:___ Structure#:____ Text:___ Inventor:____ Litigation:___ *****************
Vendors and cost where applicable

STN:________
DIALOG:______
QUESTEL/ORBIT:_____

LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:

Other(Specify):



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Run on:

Seguence:

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AC126290 Rattus no AX524297 Sequence AX524297 Sequence AX524297 Sequence AX524297 Sequence AX04425 Homo sapi AC014189 Homo sapi AK057118 Homo sapi AK057118 Homo sapi AX139070 Sequence BX51022 Zebrafish BC054676 Danio rer AJ720156 Gallus ga AX831708 Sequence AX40067 Sequence AX40067 Sequence AX59323919 Zebrafish AC113768 Rattus no AX339069 Sequence AX139069 Sequence CQ102805 Sequence
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Mus musculus
Mus rough (bouse)
Mus musculus
Musrayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1724)
1 (bases 1 to 1724)
1 (bases 1 to 1724)
Papadopoulos, V. Tobin, D., Yao, Z.X., Tasken, K. and
Papadopoulos, V. localization, and function in steroidogenesis of identification, localization, and function and PRA ralpharal-type benzodiazepine receptor- and PRA Mol. Endocrinol. 15 (12), 2211-2228 (2001)
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Li,H. and Papadopoulos,V.
Direct Submission
Direct Submission
University Medical Center, 3900 Reservoir Rd. NW, Washington, DC
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Direct Submission
Direct Submission
University Medical Center, 3900 Reservoir Rd. NW, Washington, DC 20007, USA
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On Sep 13, 2002 this sequence version replaced gi:7545290.
     AC140763
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                          AX524297
AX553035
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AC044825
AC021883
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Li, H. and Papadopoulos, V.
Direct Submission
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18.7 23076

18.7 24022

18.4 276

16.3 140409

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14.0 934

13.3 88723

10.8 1759

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9.6 1778951

8.2 198113

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7.6 554

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AB043587 Homo sapi
BC060792 Homo sapi
BC061798 Neurotran
AY150218 Homo sapi
AG194563 Homo sapi
AJ720620 Gallus ga
AY644721 Sus scrof
AK677275 Sequence
CQ714948 Sequence
BD242865 Secreted
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BC083877 Rattus no
                                                                               August 22, 2005, 17:58:08; Search time 6433 Seconds (without alignments) 10989.610 Million cell updates/sec
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Compugen Ltd.
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             GenCore version
Copyright (c) 1993 - 2005
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Listing first 45 summaries
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BC060602.1 GI:38197725
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D., Altschul, S.F., Zoeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Datchenko, L., Matusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
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996 ATCATTGCCTGCATCATCAAAGGTGAACACAGCTGGAGCAAGTGATAAACACTCTCAGTTAA
                                                                                                                                1056 TGGACAGGCCAAAACCCACACTGAAAATTCCGAAAAAGTCCTTGAGCCAGAAGGAGCTGCAGA
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LINKCCPLLSAYVASHRIEKEEEEKRRKAEEERRQREEERRLGKEEEERR
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AKTHTENSEKVLEPBAAEBALBNGPKOSLPVIAAPSWWTRPOIKDFKEKIRODADSVI
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                                                                                                                        61. .1638
/gene="Pap7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1339; DB 10;
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0; Mismatches 15;
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1. .1724
Location/Qualifiers
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Best Local Similarity 98.9%;
Matches 1348; Conservative
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                                                                                                                                                            AATAAAAGATGGCAAAGCCTTTCATCCAACTTATGAAGAAAAACTGAAGTTCGTGGCACT 349
                                                                                                                                                                                                              GCATAAGCAAGTTCTTTTGGGCCCATATAACCCAGACACGTCCCCTGAGGTTGGATTCTT 216
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                                                Length 3405;
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                                                                                                                              AGTAAAAGATGGCAAAGCCTTTCATCCAACTTATGAAGAAAAACTGAAGT
                                                                                        16; Indels
                                                  DB 10;
                                              Score 1337.4;
Pred. No. 0;
0; Mismatches
                                                91.7%;
                                                                                          Conservative
                                              Query Match
Best Local Similarity
Matches 1347; Conserv
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Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKerran, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.W., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakeeley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.N.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J. B., Jones, S.J. and Marra, M.A.
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YSLWRSKSVYYRVYYTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thomas L. Casavant.

Web site: http://genome.uiowa.edu
Contact: bento-soares@uiowa.edu;
Bonaldo,W.F., Akabogu,I., Bair,J., Crouch,K., Davis,A.,
Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dr.
                                                                                                                                                                                                                                                                                                     Straubberg, R.
Direct Submission
Submitted (31-OCT-2003) National Institutes of Health, Mammalian Submitted (31-OCT-2003) National Institutes of Health, Mammalian Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov Series: Plate: Row: Column: 0.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and
                                                                                                                                                                                                                           human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                              TITLE
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AUTHORS
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EEBEBEBUVTCEEKAKKAVNKPLLDBIVPVYRRDCHBEVYAGSHQYPGRGVYLLKFDN SYSLWRSKSVYYRVYYTR" ORIGIN	Query Match 82.5%; Score 1203.2; DB 10; Length 3461; Best Local Similarity 93.6%; Pred. No. 1.1e-298; Matches 1278; Conservative 0; Mismatches 83; Indels 5; Gaps 2;	OY 97 AGTAAAAGATGGCAAAGCCTTTCATCCAACTTATGAAGAAAAACTGAAGTTCGTGGCACT 156	Oy 157 GCATAAGCAAGTTCTTTTGGGCCCATATAACCCAGACACGTCCCCTGAGGTTGGATTCTT 216	Qy 217 TGATGTGTTGGGGAATGATGGGGGGGGAATGGGCAGCTCTGGGAAACATGTCCAAGGA 276	Oy 277 GGATGCCATGGTAGAGTTTGTGAAGCTTCTAAATAAGTGTTGTCCTCTCCTCTCGGCATA 336	Qy 33.7 TGTTGCGTCCCACAGAATAGAGAAGAAGAAGAAAGAAAGA	Oy 397 GCGAAGGCGGGGGAAGAAGAACGAGGGGGCTGCAAAAGGAAGAAGAAGAAGAAGAAA 456 	Qy 457 GCGAGAGGAGGAAGAACCCGCTGAGACGGAGGAGGAAGACAGGCGGCGCGATAGAGGAAGA 516 Db 694 GCGAGAGGAGGAGCACCGACTCAGACGGGAGGAAGAGAGAG	Qy 517 GAGGCTTCGGCTGGAACAGCAAAAGCAGCAGATAATGGCAGCTTTAAACTCGCAGACTGC 576	Qy 577 CGTGCAATTCCAGCAGTATGCAGCCCAGCAGCAACTACGAACAACAACAACAACAA 636 Db 814 CGTGCAATTCCAGCAGTATGCGGCCCAGCAGTATCCAGGAACTACGAGCAGCAGAAT 873	Oy 637 TCTCATCCGCCAGCTGCAGGAGCAGCACTATCAGCAGTATAAACACCAGGCAGAGCAAAC 696	Qy 697 CCRACCTGCACAACAGGCAGTTACAGAACGAGCAAGTAGTGATGGCTGGGGG 756 Dh 934 CCAGCTTGCAACAACAGCAATTGCAGAACGAGCAAGAAGTAGTGGCTGGC	757 ATCATTGCTGCATCATCATCATCATCATCATCATCATTAA	994 TTCATTGCCTCACGCCAGGTGAAGGTGAACGGCAGCAGCAGCAGCGCAGCAGCGAGCAGCAGCAGC	OY BIY TGGACAGGCCAAAACCCACACTGAAAATTCCGAAAAAGITCTTGAGCCAGAAGGCGGAAA B	Qy 877 AGAAGCCTTGGAAAATGGACCAAAAGACTCTTCCAGTCATTGCAGCTCCATCCA	Qy 937 GACAAGACCACAAATCAAAGACTTTAAAGAGAAGATTTCGGCAGGATGCAGATTCTGTGAT 996 Db 1174 GACAAGACCACAGATCAAAGACTTTAAAGAGAATTCGGCAGGATGCAGATTCTGTGAT 1233	997 TACAGTACGTCGAGAGAGAGTCGTCACCGTCCCGACTCCTGACGAAGGAACGATCATA 105	Db 1234 TACAGTCCGGCGAGGAGAAGTAGTCACCGTTCGAGTCCCCACTCATGAGGAAGGA
Qy 1117 GACAGACTCTCCAAATGCTGTCAGTGTGCATGTCAGTGAGTCCAGTGACGAGGAGGA 1176 Db 1310 GACAGACTCTCCAAATGCTGCTGTTGTGAATGAGTGAGTG	1177 GGAGGAGGAAGAAATGTCACTTGTGAAGAAAAAGCAAAAAAGAAGGCAAAAGAAGCCTCT 1370 GAAGGAGAAAAGAAATGTCACTTGTGAAGAAAGAAGAAAGA	1237 GCTGGATGAGATTGTACCTGTGTACCGGCGGACTGTCACGAGGAAGTATATGCAGCAG 129	1297 CCACCAGTATCCAGGAGGGGGGGGTCTATCTCCTCAAGTTTGATAATTCCTACTCTTGTG 135	141	1417 CCGGAGTCCAGGGTTGAGCACAACATGACGTTTAATTTCCTTT 1459	SULT 3	LOCUS AY336075 3461 bp mRNA linear ROD 27-JUL-2003 DEFINITION Rattus norvegicus DMT1-associated protein mRNA, complete cds. ACCESSION AY336075 VERSTON AY336075	Rattus norvegicus (Norway rat)	r e		REE	TITLE Direct Submission JOURNAL Submitted (03UL-2003) Feist-Weiller Cancer Center, LSU Health Sciences Center, 1501 Kings Highway, Shreveport, LA 71105, USA FRATURES	й		CDS 591639 /note="golgi resident protein GCP60; peripherial benzodiazapine receptor-associated protein; golgi	(RIalpha) -associated protein; DAP" / codon start=1 / product="DMT1-associated protein"	/protein_id="AAP94639_1" /db_xref="Gi:33114045" /translation="WAAQLNVEQLEVSLDGLTLSPDSEERPGAEGAPLQTPPSSPPRD GLGSGTAGQQREPGEAAAEGAAEEARRMEQHWGFGLEELYGLARFYKIKDGKAFHPT	Y BEKLKFYALHKOVLLAPYNDPIYSPEVGFPOVLGNRRRBRAALGMRKEDAMVEFYK LLNKCCPLLSAYVASHRI BKEREEKKRKAREEERRQREEERERRJOKEEEKRKREEEDR LRREEEERRRI EEERLRLEQOKQQIMAALNSQTAVQFQQYAAQQYPGNYEQQOLLIRQ	LGEGHYQQYMQQLYQVQLAQQQAALQKQGEVVVAGASLPASTKVNYAGASDPLÞVNGQ AKTHTENPEKVLEPEAAEEALENGPKDSLPVIAAPSMWTRPQIKDFKEKIRQDADSVI TVRRGEVVTVRVPTHEEGSYLFWEFATDSYDIGFGVYFEWTDSPNAAVSVHVSESSDD

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Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Translation="MAAQLNYBQLEVSLDGLTLSPDSEERPGAEGAPLQTPPSSPPGD
GLGSGTAGQQREPGEAAAEGAAEEARRMEQHWGFGLEBLYGLALRFYKIKDGKAFHPT
SEEKLKKYAHKQVLLGPYNPDTSPBCFPVLGAMAALGNNSKEBAAALGNNSFVK
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LRRBEBERRRIBEREBEKRKAEEBRROQREERRELQKEBEKKRKGEBD
LRRBEBERRRIBERGOKQQIMAALNSQTAVQFOQYAAQQYPGNYBQQQILIRQ
LQBQHYQQYMQQLYQVQAQAQASALDKAASALPAAKWYNTAGAGPBLPVNGG
AKTHTENPEKVLEPPBAAELBNGPKOSLPVIAAPSMYTRPQIKDFKEKIRQDADSVI
TVRRGEWVTVRVPPTHEGSYLLFWERATDSYDIGFGYYFEMTDSPNAAVSVHYSESSDD
EREEEBERNYTCEEKAKKNNKPLLDBIVPVYRRDCHEEVYAGSHQYPGRGVYLKFDN
                                                                                                                                                                                                                                                                                        found
                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 184 Row: h Column: 2
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 33469058.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295 AATAAAAAGATGGCAAAAGCCTTCCATCCAACTTACGAAGAAAAAACTGAAGTTTGTGGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 GCATAAGCAAGTTCTTTTGGGCCCATATAACCCCAGACACGTCCCCTGAGGTTGGATTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue type="Kidney, rat (Brown Norway)"
/clone Tib="NIH MGC_236"
/lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'product="DMT1-associated protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
82.3%; Score 1200.4; DB 10
Best Local Similarity 93.4%; Pred. No. 5.2e-298;
Matches 1276; Conservative 0; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="Acbd3"
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20._.1600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pExpress1"
       smail: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="Acbd3"
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Klausmer, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Haich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, W.M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwant, P.J.,
MCKernan, K.J., Malek, J.A., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muany, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butferfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marza, M.A.
Generation and initial analysis of more than 15,000 full-length
1233
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Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (01-0CT-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                          GGAGGAAGAAGAAGAAATGTCACTTGTGAAGAAAGCCAAAAAGAATGTCAACAAGCC
                                                                                                                                                                                                                                                                                   TCTGCTGGATGAGATTGTACCTGTGTACCGGCGGGACTGTCACGAGGAAGTATATGCAGG
                                                                                                                                                                                                                                                                                                                CAGCCACCAGTATCCAGGGAGGGGAGTCTATCTCCTCAAGTTTGATAATTCCTACTCT
                                                                               GACAGACTCTCCAAATGCTGCTGTCAGTGTGTCAGTGAGTCCAGT----GACGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                     1534 CAGCCACCAGTACCCAGGGGGGGGCTCTATCTCCTCAAGTTTGATAACTCCTACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BCO83877 1927 bp mRNA linear ROD 12-(
Rattus norvegicus DMT1-associated protein, mRNA (cDNA clone
MGC:95164 IMAGE:7130229), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1414 GGTCCGGAGTCCAGGGTTGAGCACAACATGACGTTTAATTTCCTTT 1459
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Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Norway rat)
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12477932
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VERSION
KEYWORDS
SOURCE
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JOURNAL
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BC083877
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COMMENT
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7

354 216

276 414

474

336

534

396

PRI 13-SEP-2003

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Substance 1. Sazuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T., Shibahara, T., Tanaka, T. and Nakamura, Y. Shibahara, T. Tanaka, T. and Nakamura, Y. Shibahara, T. Tanaka, T. and Nakamura, Y. Direct Submission

Submitted (19-840g-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-maii:flacdma@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)

NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5- & 3-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGSGRCPGASGROPPEPCBAAAGGAAEEARRILEQRWGFGLEELYGLALRFFKEEGGKAF
HPTYEEKLKLVALHKQVLMGPYNPDTCPEVGFFDVLGNDRRREWAALGNMSKEDAMVE
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SDDDEBEEERIGCERRAKKAANKPLLDEIVWYRRDCHEEVYAGSHQYPGRGVYLLKF
DNSYSLWRSKSVYRVYTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MAAVLNAERLEVSVDGLTLSPDPEERPGAEGAPLLPPPLPPPSP/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTAAAAGATGGCAAAGCCTTTCATCCAACTTATGAAGAAAAACTGAAGTTCGTGGCACT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCATAAGCAAGTICTTATGGGCCCATATAATCCAGACACTTGTCCTGAGGTTGGATTCTT 452
                                                                                                                                                                                                                          Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S. NEDO human cDNA sequencing project Unpublished
                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCATAAGCAAGTTCTTTTGGGCCCATATAACCCAGACACGTCCCCTGAGGTTGGATTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1079.6; DB 9; Length
Pred. No. 7e-267;
); Mismatches 174; Indels
                                       2140 bp mRNA linear FLJ21867 fis, clone HEP02419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="HEP02419"

/cell_line="HepG2"

/cell_type="hepgatoma"

/clone_lib="HEP"

/note="cloning vector pME18SFL3"
                                                                                                             oligo capping; fis (full insert sequence)
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
74.0%; Scc
Best Local Similarity 87.2%; Pre
Matches 1184; Conservative 0;
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/product = "ACBD3 protein"
/brotein id="AAH60792.1"
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HPTYEEKLKLYALHKKOYLMGPYNPDTCPEVGFPDVLGNDRREBANGLGNMSKEDBANDF
FVKLLANRCCHLRSTYVASHKIEKEEGEKRRKEEEERRRREEEERRELQKEEEEKRREE
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                                                                             found
                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 133 Row: 1 Column: 24
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 15826851.
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/gene="ACBD3"
/note="ACBP; Region: Acyl CoA binding protein"
/db_xref="CDD:pfam00887"
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Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A.,
R. M.
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/tissue type="Brain, hippocampus"
/clone_lib="NNH MGC_95"
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Pred. No. 1.9e-266;
0; Mismatches 175;
                                                                                                                                                                                                                                                                                                                                             'note="Vector: pBluescript"
                                                                                                                                                                                                                                                                                                                                                                                            /note="synonyms: GCP60, I
/db_xref="LocusID:64746"
/db_xref="MIM:606809"
                                                                                                                                                                                                            organism="Homo sapiens"
                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
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/codon_start=1
/product="ACBD3 p
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/gene="ACBD3"
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Best Local Similarity 87.1%;
Matches 1183; Conservative (
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                                                                                  TCTCATCCGCCAGCTGCAGGAGCAGCACTATCAGCAGTATAAACACCAGGCAGAGCAAAC
                                                                                                                                                  CCAACCTGCACAAACAAGCAGCATTACAGAAACAGCAAGAAGTAGTGATGGCTGGGGC
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

I (bases 1 to 1481)

Baughn, M.R. and Patterson, C.

Neurotransmission associated proteins
No 19 2002519064-A/3

PROTECTION-2002

PROCULL-1999 JP 2000558211

PROCULL-1999 US 60/091677

CONTAL/105,

PROCULE MOS 998868

FR Key

Location/Qualifiers

FT SOURCE MOS 998868

FT SOURCE MOS 998868
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/organism='Homo sapiens (human)'
Location/Qualifiers
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               BD261678 1481 bp DNA Neurotransmission associated proteins. BD261678
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                             BD261678.1 GI:33071446
                                                                             JP 2002519064-A/3.
Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                           971 TTCCTTGCCTACATCATCAAAAGTGAATGCAACTGTACCAAGTAATATGATGCCGGTTAA
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                                                 CGTGCAGTTCCAGCAGTATGCAGCCCAACGGTATCCAGGGAACTACGAACAGCAAAT
                                                                                             TCTCATCCGCCAGCTGCAGGAGCAGCACTATCAGCAGTATAAACACCCAGGCAGAGCAAAC
                                                                                                                                851 TCTCATCCGCCAGTTGCAGGAGCAACACTATCAGCAGTACATGCAGCAGTTGTATCAAGT
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PGSGRGPGASGEQPEPGEAAAGGAAEEARRLEQRWGFGLEELYGLALRLFKEKDGKAF
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FYLLANGCOLLESTYNAALKIEKEBOOKKRKEEBERRREKGEBERREKGEBEKREKEE
FERLERBEERER IN EIEBERLALESOCKOOIMAALNSGTAVOFOOYAAORY PGNYEOCOLI
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SDDDEEEEENIGCEEKAKKNANKPLLDEIVPVYRRDCHEEVYAGSHQYPGRGVYLLKF
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                                                                                                 Gene 308, 1-10 (2003)
2 (bases 1 to 3572)
Liu,J., Tobin,D., Tasken,K. and Papadopoulos,V.

Direct Submission
Submitted (13-SEP-2002) Department of Cell Biology, Georgetown Univ./Medical Center, 3900 Reservoir Rd. NW, Washington, DC 20057, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3572)
Liu,J., Cavalli,L.R., Haddad,B.R. and Papadopoulos,V. Molecular cloning, genomic organization, chromosomal mapping a subcellular localization of mouse PAP7: a PBR and PKA-Rialpha associated protein
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/organise="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:9606"
/fissue_type="placenta"
27. .1613
/note="PAP7; PBR associated protein"
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Pred. No. 1.6e-260;
0; Mismatches 175;
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KRREREEBERRR IEBERKLELGOKOOIMAALNSOTAVOPOOYAAQOYDGNY
BOQOILIROLOEGHYVOOYMOLYOVOLAQOQAALOKOOEVVVAGSSLPTSSKVNATVE
SNMMSVNGQAKTHTDSSEKELBEPAAREALENGPKESLPVIAAPSMWTRPQIKOFKEK
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VHVSESSDDDEEEERNIGCEEKAKKNANKPLLDEIVVARDCHEEVYAGSHQYPGRG
VYLLKFDDNSYSLWRSCVYTRVYTR"
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                                                                                                                                                                                                                                     Length 3037;
                                                                                                                                                                                                                                   Score 890; DB 9; Length 30
Pred. No. 5.1e-218;
0; Mismatches 155; Indels
                                                                                                                                                                                                                                   61.0%;
86.4%;
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Mammalia, Eutheria, Primates; Catarrhini, Hominidae; Homo.

Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Rlaugner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.J., Mullahy, S.J., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

L. Park, Med. Sci. U.S., 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LiNL at: http://image.llnl.gov Series: IRAK Plate: 21 Row: c Column: 15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (24-UUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaztne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WIH-MGC Project URL: http://mgc.nci.nih.gov
On Sep 16, 2003 this sequence version replaced gi:21961496.
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Prayaed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Baylor College of Medicine Human Genome
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/db_xref="LocusID:64746"
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/gene="ACBD3"
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Center code: BCM-HGSC
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                              REFERENCE
AUTHORS
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AUTHORS
TITLE
JOURNAL
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PUBMED
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                                                                                                                                         Gaps
                                                                                                                                       9
                                                                                                      Length 3492;
                                                                                                  Score 865.8; DB 5; Length
Pred. No. 9e-212;
0; Mismatches 262; Indels
                             1611. .>3492
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                                                                                                    59.3%;
79.5%;
                KTVYYRVYYTR
                                                                                                  Query Match
Best Local Similarity 79.5'
Matches 1039; Conservative
                                                                                                                                                                                                         303
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AJ720620
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Gallus gallus
Gallus gallus
Kataryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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Submitted (20-MAY-2004) Caldwell R.B., GSF - Forschungszentrum,
Institut fuer Molekulare Strahlenbiologie, Ingolstaedter Landstr.
1, D-8574 Neuherberg, GERMANY
Location/Qualifiers
1. 3492
            AAGAACGCCAACAAGCCTCTGCTGGATGAGATTGTACCTGTGTACCGGCGGGACTGTCAC
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                                                                                AAGAATGCCAACAAGCCTTTGCTGGATGAATTGTGCCTGTGTACCGACGGGACTCTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caldwell, R.B., Kierzek, A.M., Arakawa, H., Bezzubov, Y., Zaim, J., Fiedler, P., Kutter, S., Blagodatski, A., Kostovska, D., Koter, M., Plachy, J., Carninci, P., Hayashizaki, Y. and Buerstedde, J.M. Full-length CDNAs from bursal lymphocytes to facilitate gene function analysis
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Caldwell, R.B.
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BYDSPNTANSVSVHYSESSEHDDEEEERNISSERAKKNANKFVLDEIVPVYRRDCHEE

VYAGSHQYPGRGYYLKFDNSYSLWRSKSVYTRYTR"
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AX644721. GI:49615356
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1 (Dases 1 to 1598)

Zhang, K., Petit-Paris, I., Dutheil, D., Favreau, F., Tallineau, C., Milan, D., Mauco, G., Papadopoulos, V. and Haue, T.

Direct Submission
Submitted (04-JUN-2004) Inserm ERM 324, Renal Ischemia Reperfusion and Transplantation, Faculte de Medecine et Pharmacie/CHU de Poitiers, Rue de Le Miletrie, B.P. 577, Poitiers, Cedex 86021, France
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Pred. No. 4.6e-210;
0; Mismatches 170; Indels
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147. .1265
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1039 TCATGAGGAAGGATCATACCTATTTTGGGAATTTGCCACAGACAG	Db 661 TGGGGTGTATTTTGAATGGACAGACTCTCCAAACACTGCTGTCAGTGA 720	RESULT 14 CQ714948 LOCUS CQ714948 LOCUS CQ714948 ACCESSION CQ714948 VERSION CQ714948 VERSION CQ714948.1 GI:42275805 KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens Elkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia: Putheria: Primates: Catarrhini: Hominidae: Homo.	Venter, C.J., Adams, M.C., Li, P. Vits, such as nucleic acid arihumanexons or transcripts, for thereof Patent: WO 02068579-A 882 06-5 PE Corporation (WY) (US) Location/Qualifiers	source 1se / Organism="Homo sapiens" / Mol Lype="unassigned DNA" / Mol Lype="unassigned DNA" / Mol Xref="taxon:9606" / Mol Xref="taxon		Qy 661 GCACTATCAGCAGTATAAACACCAGGCAGACAAACCCAACCTGCACAACAGGCAGC 720 L1
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C12P19/34//(C12P19/34,C12R1:91),C12N1S/00,C12NS/00,A61K37/02
Secreted proteins and polynucleotides encoding them FH Key
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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OS HGMC sapiens (human)
PN 47 2002536973-A/16
PN 55-NOV-2002
PF 18-FEB-2000 JP 200599860
PR 19-FEB-1999 US 60/120680,23-APR-1999 US 09/298733 PR 17-AUG-1999 US 60/157247,29-NOV-1999 US 60/157823 PR 29-NOV-1999 US 60/167823 PR 29-NOV-1999 US 60/167823 PR 29-NOV-1999 US 60/167823 PR 29-NOV-1999 US 60/167822 PR 29-NOV-1999 US 60/167828 PR 20-NOV-1999 US 60/16788 PR 20-NOV-1999 US 60/167821 PR 20-NOV-1999 US 60/167828 PR 20-NOV-1999 US 60/167878 PR 20-NOV-1999 US 60/167878 PR 20-NOV-1999 US 60/167878 PR 20-NOV-1999 US 60/167878 PR 20-NOV-1999 US 60/16788 PR 20-NOV-1999 US 60/1678 PR 20
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JP 2002536973-A/16.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2714)
Valenzuela,D., Yuan,O., Hoffman,H., Hall,J. and Rapiejko,P.
Secreted proteins and polynucleotides encoding them
Patent: JP 2002536973-A 16 05-NOV-2002;
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AGIP31/12,
AGIP31/18, AGIP31/20, AGIP31/22, AGIP37/00, AGIP37/06, C07K14/435,
                                                                                          CAGCTCCGAAAAAGAACTGGAACCAGAAGCTGCAGAAGAAGAAGCCCTGGAGAATGGACCAAA
                                                                                                                                                                 AGAATCTCTTCCAGTAATAGCAGCTCCATCCATGTGGACACGACCTCAGATCAAAGAACTT
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                                             841 AAATTCCGAAAAAGTCCTTGAGCCAGAAGCTGCAGAAGAAGACCTTGGAAAATGGACCAAA
                                                                                                                                       AGACTCTCTTCCAGTGATTGCAGCTCCATGTGGACAAGACCACAAAATCAAAGACTT
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Search completed: August 22, 2005, 22:24:27 Job time : 6440 secs

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Aah72906 Human cer Aak7371 Human imm Abk24345 DNA encod Aai17988 Probe #79 Aba62955 Human foe Aai43978 Probe #11 Aak37154 Human bon

Human

Aak11364

AA117988 ABA62955 AA142978 AAX37154 AAX11364 ABS36831 ABS11145

Abs36831 Human 11v Abs11145 Human gen Adg1897 Human gen Ada17184 Probe #18 Abs76496 Human foe Aa157184 Probe #25 Aa451149 Human bon Aa45149 Human bon Abs26709 Human liv Abs24667 Human gen Abs24667 Human gen Abs25196 Human con Abs35196 Human con

ABA76496 AAI57184 AAK51149

Adq97348 Mouse car

ALIGNMENTS

ADQ97348

ADQ97654 ABV55196

AAK25143 ABS50709 ABS24667 ABL24635

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Peripheral-type benzodiazepine receptor; PBR; PBR- associated protein; PAR; cell proliferation; cancer; cell death; cytostatic; neuroprotective; immunomodulator; antiinfertility; cerebroprotective; atherosclerosis; Niemann-Pick C; tumour; Alzheimer's disease; developmental disorder; cholesterol; multiple sclerosis; stress; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel peripheral-type benzodiazepine receptor associated proteins used for the regulation of the peripheral-type benzodiazepine receptor.
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8. .1399
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/product= "PAP7"
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        The invention provides isolated peripheral-type benzodiazepine receptor

(PBR) associated proteins (PAPB) and nucleic acids encoding the PAP

proteins. The PAP polynucleotides are a source of primers and probes for

detection, isolation and amplification. PAP ligands or substrates or

antibodies can be labeled and used to detect PAPB, in the diagnosis and

prognosis of disease associated with increased cell proliferation, such

as cancer, or reduced cell death. The diagnostic methods of the invention

can be predictive of diseases involving PBR including gallstones,

atherosclerosis, Niemann-Pick C, Sitosterolemia, Dystrophy, tumor

proliferation, Schnyder's corneal crystalline dystrophy, brain disorders

including Alzheimer's disease, cholesterol methodism, Tellurium

toxicity, Smith-Lemli-Opitz syndrome, myelinization, developmental

conscity, Smith-Lemli-Opitz syndrome, myelinization, developmental

conscity, Smith-Lemli-Opitz syndrome, or in screening for compounds

cuseful in prophylactic treatment, or in screening for compounds

effective in prophylactive treatment. The PAPS may be used to identify

capents which modulate PBR activity. Inhibitors of PAP may be used in the

treatment or amelloration of conditions such as stress and stroke,

cancer, neurodegenerative disorders, developmental and stroke,

cancer, or neurodegenerative disorders, developmental and stroke,

cancer, neurodegenerative disorders, developmental and stroke,

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cancer, cancer, cancer, cancer, cancer, cancer, infertility
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The invention Figures to an isolated, purilled or recombinant complex (1) comprising a PoSH polypeptide and a PoSH-associated protein (PoSH-AP) (a) or HERPUDI and a Ubiquitin ligase (b). Methods using (1), (a) or (b) are useful for identifying an agent that modulates an activity of a PoSH polypeptide or POSH-AP, for identifying an antiviral agent, an anti-apportit agent, an anti-cancer agent, an agent that inhibits trafficking of a protein through the secretory pathway, an agent that inhibits the progression of a neurological disorder, an agent that modulates a PoSH function, an agent that modulates a PoSH cured for treating a viral infection, for inhibiting an activity of a PoSH-associated disease is viral infection, PoSH-associated cancer or PoSH-associated disease is viral infection, PoSH-associated cancer or treating or preventing PoSH-associated meriodical disorder. The methods are useful for treating or preventing PoSH-associated meurological disorder. The methods are useful for treating or preventing PoSH-associated meurological disorder in a subject corresponds to a chizophrenia, Neimann-Pick's disease, Huntington's disease, and sease, Parkinson's disease, Huntington's disease, and sease, Parkinson's disease, This sequence corresponds to a Isolated, purified or recombinant complex, useful for identifying an antiviral, anti-apoptotic or anti-cancer, comprising POSH polypeptide and POSH-associated protein (POSH-AP). invention relates to an isolated, purified or recombinant complex (1) vrising a POSH polypeptide and a POSH-associated protein (POSH-AP) (a) ŝ Tuvia neurological disorder progression disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; schizophrenia; Niemann-Pick's disease. Sequence 2140 BP; 628 A; 461 C; 587 G; 464 T; 0 U; 0 Other; Ben-Avraham D, Yaar L, Disclosure; SEQ ID NO 49; 374pp; English. DN, Alroy I, Reiss Y, 2003US-0464285P. 2003US-0469462P. 2003US-0471378P. 2003US-0472327P. 2003US-0474706F. of the invention 2003US-0455760P. 2003US-0456640P. 2003US-0460526P. 2003US-0480215P. 2003US-0480376P. 2003US-0493860P. 02-MAR-2004; 2004WO-US006308 2003US-0460792P 2003US-0479317P 2003US-0498634P 2003US-0503931P. 2003WO-US035712. 2004WO-US003600. 2004US-0549896P (PROT-) PROTEOLOGICS INC WPI; 2004-662346/64. WO2004078130-A2 19-MAR-2003; 20-MAR-2003; 03-APR-2003; 21-APR-2003; 09-MAY-2003; 15-MAY-2003; 04-APR-2003; 20-MAY-2003; 30-MAY-2003; 19-JUN-2003; 16-SEP-2003; acid sapiens 17-JUN-2003; 28-AUG-2003; 02-MAR-2004; 05-FEB-2004;

AGTAAAAGGTGGCAAAGCCTTTCATCCAACTTATGAAGAAAAACTGAÄGTTCGTGGCACT Gaps 74.0%; Score 1079.6; DB 13; Length 2140; 87.2%; Pred. No. 6.1e-281; ive 0; Mismatches 174; Indels 0; Conservative Query Match Best Local Similarity Matches 1184; Conserv 97

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1056 1352 1052 TGGACAGGCCAAAACACACACTGACAGCTCCGAAAAAGAACTGGAACCAGAAGCTGCAGA 1112 1232 336 452 512 396 632 456 692 516 752 576 812 636 872 756 816 333 AGAAAAAGATGGCAAAGCATTTCATCCAACTTATGAAGAAAATTGAAGCTTGTGGCACT 392 GCGAAGGCGCGTGAAGAGAAAAACGAAAACGTCTGCAAAAGGAGAAGAAGAAGAAGTAG GCATAAGCAAGTTCTTTGGGCCCATATAACCCAGACACGTCCCCTGAGGTTGGATTCTT GCATAAGCAAGTTCTTATGGGCCCATATAATCCAGACACTTGTCCTGAGGTTGGATTCTT TGATGTTGGGGAATGATAGGAGAGAGAATGGGCAGCTCTGGGAAACATGTCCAAGGA TGATGTTGGGGAATGACAGGAGAGAGAATGGGCCAGCCTGGGAAACATGTCTAAAGA GGATGCCATGGTAGAGGTTTGTGAAGGCTTCTAAATAAGTGTTGTCCTCTCCTCTCGGCATA GGATGCCATGGTGGAGTTTGTCAAGCTCTTAAATAGGTGTTGCCATCTCTTTTCAACATA GCGAAGGCAGCGTGAAGAGGAAGAACGAGAGCGCCTGCAAAAAGGAAGAAGAAGAAGCGGAA AAGGCTTCGGTTGGAGCAGCAAAAGCAGCAGATAATGGCAGCTTTAAAACTCCCAGACTGC CGTGCAATTCCAGCAGTATGCAGCCCAGCAGTATCCAGGGAACTACGAACAACAGCAGAT CGTGCAGTTCCAGCAGTATGCAGCCCAACAGTATCCAGGGAACTACGAACAGCAGCAAAT TCTCATCCGCCAGCTGCAGGAGCAGCACTATCAGCAGTATAAACACCCAGGCAGAGCAAAC CCAACCTGCACAACAACAGCAGCATTACAGAAACAGCAAGAAGTAGTGATGGCTGGGGC 1173 GACACGACCTCAGATCAAAGACTTCAAAGAGAAGATTCAGCAGGATGCAGATTCCGTGAT GAGGCTTCGGCTGGAACAGCAAAAGCAGCAGATAATGGCAGCTTTAAACTCGCAGACTGC ATCATTGCCTGCATCATCAAAGGTGAACACAGCTGGAGCAAGTGATACACTGTCAGTTAA TTCCTTGCCTACATCATCAAAAGTGAATGCAACTGTACCAAGTAATATGATGTCAGTTAA 1293 TCTCTTTTGGGAATTTGCCACAGACAATTATGACATTGGGTTTGGGGTGTATTTTGAATG TGGACAGGCCAAAACCCACACTGAAAATTCCGAAAAAGTCCTTGAGCCAGAAGCTGCAGA AGAAGCCTTGGAAAATGGACCAAAAGACTCTTCCAGTGATTGCAGCTCCATGTG 1057 CCTATTTTGGGAATTTGCCACAGACAGTTATGACATTGGGTTTTGGGTTTTTGAATG GACAGACTCTCCAAATGCTGCTGTCAGTGTGCATGTCAGTGAGTCCAGTGACGAGGAA GACAAGACCACAATCAAAGACTTTAAAGAGAAGATTCGGCAGGATGCAGATTCTGTGAT 933 993 817 1053 937 266 1233 157 393 217 453 513 573 397 457 693 517 753 577 813 877 1117 277 337 633 637 873 697 757 1353 1177 원 g ઠે 요 В g 엄 ò ò Š ઠે 유 ò à 셤 ò ò 유 ò 셤 g 임 셤 셤 ò ઠે ò ò 요 8 8 à 임 8

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357 GCATAAGCAAGTTCTTATGGGCCCATATAATCCAGACACTTGTCTGTGTGGATTCTT 416
treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
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                                               CCATCAATATCCAGGGAGAGAGTCTATCTCCTCAAGTTTGACAACTCCTACTTTTGTG
                   Asundi V, Zhou P, Xu C, Cao Y;
J, Zhang J, Ren F, Chen R, Wang
Goodrich R;
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27-APR-2000; 2000US-00560875.
20-JUN-2000; 2000US-00598075.
19-JUL-2000; 2000US-005328.
01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-00653551.
20-OCT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00593325.
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hao QA, Wang D, Wang
Yang Y, Wejhrman T,
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Ma Y, Zh
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                                       CCTATITITGGGAATITIGCCACAGACAGITATGACATITGGGTTTTGGGGTTTTATTTTGAATG
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2003US-0475825P.
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2003US-0480215P.
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2003US-0455760P.
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2003US-0469462P.
2003US-0471378P.
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2003US-0460526P.
2003US-0460792P.
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15-MAY-2003;
20-MAY-2003;
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03-JUN-2003;
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The invention relates to an isolated, purified or recombinant complex (I) comprising a POSH polypeptide and a POSH-associated protein (POSH-AP) (a) or HERPUDI and a Ubiquitin ligase (b). Methods using (I), (a) or (b) are useful for identifying an agent that modulates an activity of a POSH polypeptide or POSH-AP, for identifying an antiviral agent, an anticancer agent, an anti-cancer agent, an agent that inhibits trafficking of a protein through the secretory pathway, an agent that inhibits the progression of a neurological disorder, an agent that inhibits the progression of a neurological disorder, an agent that inhibits can be used for treating a viral infection, for inhibiting an activity of a POSH-associated disease is viral infection, for inhibiting an activity of a POSH-associated disease is viral infection, POSH-associated cancer or POSH-associated disease is viral infection, POSH-associated cancer or treating or preventing POSH-associated neurological disorder in a subject treating or preventing POSH-associated neurological disorder in a subject c. c.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, Schizophrenia, Niemann-Pick's disease. This sequence corresponds to a
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Pred. No. 7.9e-281;
0; Mismatches 174; Indels
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                                     28-AUG-2003; 2003US-0498634P.
16-SEP-2003; 2003US-0503931P.
10-NOV-2003; 2004WO-US035712.
05-FEB-2004; 2004WO-US03500.
2003US-0493860P
                                                                                                                                                                                         02-MAR-2004; 2004US-0549896P
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Best Local Similarity 87.2%;
Matches 1184; Conservative
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ds; gene; cytostatic; nootropic; neuroprotective; antiparkinsoni anticonvulsant; antiviral; neuroleptic; central nervous system; POSH polypeptide; POSH-AP; HERPUDI; Ubiquitin ligase; antiviral agent; anti-apoptotic agent; anti-cancer agent; secretory pathway traficking inhibitor; neurological disorder progression disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; schizophrenia; Niemann-Pick's disease.

WO2004078130-A2

Homo sapiens

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                                       CGTGCAATTCCAGCAGTATGCAGCCCAGCAGTATCCAGGGAACTACGAACAACAGCAGAT
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The invention relates to an isolated, purified or recombinant complex (I) comprising a POSH polypeptide and a POSH-associated protein (POSH-AP) (a) or HERPUDI and a Ubiquitin ligase (b). Methods using (I), (a) or (b) are useful for identifying an agent that modulates an activity of a POSH polypeptide or POSH-AP, for identifying an antiviral agent, an anticancer agent, an agent that inhibits trafficking of a protein through the secretory pathway, an agent that inhibits the progression of a neurological disorder, an agent that inhibits the progression of a neurological disorder, an agent that modulates a POSH cused for treating a viral infection, for inhibiting an activity of a POSH-associated disease is viral infection, for inhibiting an activity of a POSH-associated disease is viral infection, POSH-associated cancer or POSH-associated neurological disorder. The methods are useful for treating or preventing POSH-associated neurological disorder in a subject treating or preventing POSH-associated neurological disorder in a subject end of the post parkinson's disease, Huntington's disease, solizophrenia, Niemann-Pick's disease. This sequence corresponds to a
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05-MAR-2003; 2003US-0452284P.
19-MAR-2003; 2003US-0455560P.
20-MAR-2003; 2003US-046640P.
03-APR-2003; 2003US-046670P.
21-APR-2003; 2003US-0464285P.
21-APR-2003; 2003US-0464285P.
15-MAY-2003; 2003US-0464285P.
15-MAY-2003; 2003US-047378P.
20-MAY-2003; 2003US-047378P.
20-MAY-2003; 2003US-047378P.
20-MAY-2003; 2003US-047378P.
20-MAY-2003; 2003US-047378P.
20-MAY-2003; 2003US-047378P.
20-MAY-2003; 2003US-04738P.
20-MAY-2003; 2003US-04738P.
20-MAY-2003; 2003US-04980376P.
28-AUG-2003; 2003US-0498634P.
16-SEP-2003; 2003US-0498634P.
16-SEP-2003; 2003US-0498634P.
16-SEP-2003; 2003US-0498634P.
16-SEP-2003; 2003US-0498634P.
16-SEP-2003; 2003US-0498634P.
16-SEP-2003; 2003US-0498634P.
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antiviral, anti-apopto
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Sequence 3598 BP; 1071 A; 667 C;

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DNA; 3598

standard;

ADS34287 ADS34287;

RESULT

POSH protein associated DNA #41

(first entry)

02-DEC-2004

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87.1%; Pred. No. 2.1e-280;
tive 0; Mismatches 175;
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                                                                                                                                                                                                                                                                                                      New human neurotransmission associated proteins, useful for treatment, prevention and diagnosis of neurological disease, e.g. Alzheimer's disease, and antagonists for treating cancer or immune disorders.
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IR, Patterson C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated, purified or recombinant complex (I) comprising a POSH polypeptide and a POSH-associated protein (POSH-AP) (a) or HERRUDI and a Ubiquitin ligase (b). Methods using (I), (a) or (b) are useful for identifying an agent that modulates an activity of a POSH polypeptide or POSH-AP, for identifying an antiviral agent, an anti-appoptotic agent, an anti-cancer agent, an agent that inhibits trafficking of a protein through the secretory pathway, an agent that inhibits the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated, purified or recombinant complex, useful for identifying an antiviral, anti-apoptotic or anti-cancer, comprising POSH polypeptide
                                                                                                                                               cytostatic; nootropic; neuroprotective; antiparkinsonian;
                                                                                                                                                      anticonvulsant; antiviral; neuroleptic; central nervous system; POSH polypeptide; POSH-associated protein; POSH-AP; HERPUD1; Ubiquitin ligase; antiviral agent; anti-apoptotic agent; anti-cancer agent; secretory pathway traficking inhibitor; neurological disorder progression disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; schizophrenia;
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CTGGAGTCTAGGGTTGGGCAGAAGATGACATTTAATTT 1427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiviral, anti-apoptotic or anti-cancer, POSH-associated protein (POSH-AP).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 55; 374pp; English.
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                                                                                                                          POSH protein associated DNA #45
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2003US-0479117P
2003US-0480215P
2003US-0480376P
2003US-049864P
2003US-049864P
2003US-0503931P
2003WG-0503931P
2004WO-US003600
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2003US-0455760P.
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                                                             standard;
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09-MAY-2003;
15-MAY-2003;
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17-JUN-2003;
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16-SEP-2003;
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05-FEB-2004;
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progression of a neurological disorder, an agent that modulates a POSH function, an agent that modulates a HERPUD1 function. The methods can be used for treating a viral infection, for inhibiting an activity of a POSH-AP in a cell, for treating a POSH-associated disease in a subject. The POSH-associated disease is viral infection, POSH-associated cancer or POSH-associated neurological disorder. The methods are useful for treating or preventing POSH-associated neurological disorder in a subject e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, schizophrenia, Niemann-Pick's disease. This sequence corresponds to a
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                                                                                                                                                                                                                                                                                                                             Sequence 1995 BP; 628 A; 412 C; 549 G; 406 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                Score 1068.6; DB 13; Lengt
Pred. No. 5.6e-278;
0; Mismatches 174; Indels
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Best Local Similarity 87.1%;
Matches 1184; Conservative
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97 AGTAAAAGATGGCAAAGCCTTTCATCCAACTTATGAAGAAAAACTGGAAGTTCGTGGCACT 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3572 BP; 1067 A; 665 C; 826 G; 1013 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 72.3%; Score 1055; DB 13; Best Local Similarity 87.0%; Pred. No. 3.5e-274; Matches 1182; Conservative 0; Mismatches 175;
                                                                                                                                                                                                                        WPI; 2004-662346/64.
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              GGACACGACCTCAGATCAAAGACTTCAAAGAGAAGATTCAGCAGGATGCAGATTCCGTGA
                                              ACCTATTTTGGGAATTTGCCACAGACAGTTATGACATTGGGTTTGGGGTTTATTTTGAAT
                                                                                                          1270 AICTCTTTTGGGAATTTGCCACAGACAATTATGACATTGGGTTTTGGGTGTATTTTGAAT
                                                                                                                                             GGACAGACTCTCCAAATGCTGCTGTCAGTGTGTCAGTGAGTCCAGTGACGAGGGGGG
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GGACAAGACCACAAATCAAAGACTTTAAAGAGAAGATTCGGCAGGATGCAGATTCTGTGA
                                                                    ds; gene; cytostatic; nootropic; neuroprotective; antiparkinsonian; antioorvulasant; antiviral; neuroleptic; central nervous system; POSH polypeptide; POSH antiviral speciated protein; POSH-AP; HERPUDI; Ubiquitin ligase; antiviral agent; anti-apoptotic agent; anti-cancer agent; secretory pathway trafficking inhibitor; neurological disorder progression disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; schizophrenia;
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2003US-0460792P
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Length 3572;

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The invention relates to an isolated, purified or recombinant complex (I) comprising a POSH polypeptide and a POSH-associated protein (POSH-AP) (a) or HERPUDI and a Ubiquith ligase (b). Methods using (I), (a) or (b) are useful for identifying an agent that modulates an activity of a POSH polypeptide or POSH-AP, for identifying an antiviral agent, an anti-cancer agent, an agent that inhibits trafficking of a protein through the secretory pathway, an agent that inhibits the progression of a neurological disorder, an agent that inhibits the progression of a neurological disorder, an agent that modulates a POSH function, an agent that modulates a HERPUDI function. The methods can be used for treating a viral infection, for inhibiting an activity of a POSH-associated disease is viral infection, POSH-associated cancer or POSH-associated neurological disorder. The methods are useful for treating POSH-associated meurological disorder in a subject ceg. Alzheimer's disease, Parkinson's disease, Huntington's disease, sollicable in a subject cellizophrenia, Niemann-Pick's disease. This sequence corresponds to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated, purified or recombinant complex, useful for identifying an antiviral, anti-apoptotic or anti-cancer, comprising POSH polypeptide and POSH-associated protein (POSH-AP).
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20-MAY-2003; 2003US-0472327P.
33-MAY-2003; 2003US-0474706P.
33-JUN-2003; 2003US-0479317P.
19-JUN-2003; 2003US-0479317P.
19-JUN-2003; 2003US-0480215P.
19-JUN-2003; 2003US-0493860P.
28-AUG-2003; 2003US-0493860P.
16-SEP-2003; 2003US-0493860P.
10-NOV-2003; 2003US-0503931P.
10-NOV-2003; 2003WG-US035112.
05-PEB-2004; 2004WG-US003600.
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to ortokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, inmunomodulatory activity and activity, inmunomodulatory activity and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52581) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 395 GCATAAGCAAGTTCTTATGGGCCCCATATAATCCAGACACTTGTCCTGAGGTTGGATCTT 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cleic acids encoding polypeptides with cytokine-like activities, useful diagnosis and gene therapy.
                                                                                                        Human, cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
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J, Zhang J, Ren F,
Goodrich R;
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Pred. No. 1.1e-271;
0; Mismatches 181; I
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                                                                             polynucleotide SEQ ID NO 2564.
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27-APR-2000; 2000US-00560B75.
20-UJN-2000; 2000US-00590075.
19-JJL-2000; 2000US-00654936.
15-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-0063325.
20-OCT-2000; 2000US-0063325.
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Wejhrman T,
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Best Local Similarity 86.5%;
Matches 1177; Conservative (
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P-PSDB; AAM79902.
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Ma Y, Zhao QA,
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AAK53035 standard; cDNA; 2350

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GTGGCGGTCAAAATCAGTCTACTACAGAGTCTATTATACTAGATAAAAATGTTGTTACAA 1654
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             ds; gene; cytostatic; nootropic; neuroprotective; antiparkinsonian; antioonvulaant; antiviral; neuroleptic; central nervous system; POSH polypeptide; POSH-associated protein; POSH-AP; HERPUDI; Ubiquitin ligase; antiviral agent; anti-apoptotic agent; anti-cancer agent; secretory pathway traficking inhibitor; neurological disorder progression disorder; Alzheimer's disease; parkinson, siesese; Hutington's disease; schizophrenia;
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09-MAR-2003; 2003US-0455284P.
19-MAR-2003; 2003US-045560P.
20-MAR-2003; 2003US-0456640P.
03-APR-2003; 2003US-0460526P.
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30-MAY-2003; 2003US-047327P.
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19-JUN-2003; 2003US-0490317P.
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28-AUG-2003; 2003US-0490364P.
16-SEP-2004; 2003US-0490864P.
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                                                                                                                                      ADS34288 standard; DNA; 3049
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comprising a PoSH polypeptide and a PoSH-associated protein (PoSH-AP) (a) or HERPUDI and a Ubiquitin ligase (b). Methods using (1), (a) or (b) are useful for identifying an agent that modulates an activity of a PoSH polypeptide or PoSH-AP, for identifying an autiviral agent, an anti-apoptotic agent, an anti-cancer agent, an agent that inhibits trafficking of a protein through the secretory pathway, an agent that inhibits the protein through the secretory pathway, an agent that inhibits the progression of a neurological disorder, an agent that modulates a PoSH function, an agent that modulates a PoSH consider for treating a viral infection, for inhibiting an activity of a PoSH-associated disease is viral infection, PoSH-associated cancer or PoSH-associated disease is viral infection, PoSH-associated cancer or treating or preventing PoSH-associated neurological disorder in a subject treating or preventing PoSH-associated neurological disorder in a subject e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, schizophrenia, Niemann-Pick's disease. This sequence corresponds to a
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Pred. No. 1e-229;
0; Mismatches 156; Indels 0;
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86.3%;
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anorectic; antidiabetic; protein-protein interaction; diabetes;
yeast 2-hybrid assay; metabolic disorder; obesity.
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14-MAR-2001; 2001US-0275734P Legrain P, Daviet L; WPI; 2003-103412/09. (HYBR-) HYBRIGENICS P-PSDB; ABU70389. New complex between two interacting proteins in adipocyte cells, useful for identifying selected interacting domains that modulate protein interactions, or for preventing or treating metabolic disorders such as obesity or diabetes.

Claim 7; Page 115; 382pp; English.

The invention relates to a complex between two interacting proteins in adipocyte cells, given in the specification. The proteins are identified by selecting a bait protein from a known adipocyte marker and then performing a yeast 2-hybrid selection to isolate prey proteins encoded by members of an adipocyte cDNA library. The proteins are designated SID (RTM) (selected interacting domains) proteins. Also included are a polymucleotide encoding a polympetide in the adipocyte cells, a recombinant host cell expressing at least one of the interacting

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polypeptides of the complex, selecting a modulating compound in adipocyte cells, a SID (RTM) polypeptide comprising any of the 738 amino acid sequences given in the specification (including its fragment or variant), a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences given in the specification (including its fragment or variant), a vector comprising the Vector, a protein chip comprising the polypeptides and a record comprising the vector, a protein chip comprising the polypeptides and comprising the vector, a protein chip comprising the polypeptides and a record comprising all or part of the data, listed in the specification. The complex, polypeptides, polynucleotides and compounds are useful for preventing or treating metabolic disorders such as obesity or diabetes. The polynucleotides are useful as probes or primers. The complex is particularly useful for identifying selected interacting domains (SID (RTM)) for screening drugs that modulate the protein interaction, thus continue the therapeutic effect. The present sequence encodes a SID (Continue) and the continue of the contin
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0; Mismatches 125;
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                                                                                              | TAATICCTACTCTCTGTGGAGGTCCAAGTCCGTCTACTACAGAGTCTATATACTAGATA
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                                                                                                                                                                                                                                                                                    Human, secreted protein, cytokine, cell proliferation,
nutritional supplement, immune modulation, autoimmune disorder,
haematopoiesis regulation, tissue growth; haemostasis, inflammation;
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Human ORFX ORF2918 polynucleotide sequence SEQ ID NO:5835.

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Pred. No. 1.2e-160;
0; Mismatches 112;
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AAC77363 standard; cDNA; 420

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RESULT 14 AAC77363

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which represent the human ORFX open reading frames 1 to 3161. The ORFX equations are activities such as: cytostatic; hepatotropic; vulnerary; sequences have activities such as: cytostatic; hepatotropic; vulnerary; antiporiatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; incorropic; neuroprotective; osteopathic; cardiant; thrombolytic; cagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antithenmalic; antithyroid; antidiabetic; hypotensive; correcting or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegemerative cused to treat cancers, proliferative disorders, neurodegemerative clasorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester compliance systemic lupus erythematosus, severe combined immunodeficiency
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease;
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                                                                                                                                       open reading frame; ORFX; detection; cytostatic; hepatotropic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enhance coagulation; to inhibit thrombosis; and as a contraceptive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
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02-APR-1999; 99US-0127636P.
05-APR-1999; 99US-01277289.
30-MAR-2000; 2000US-00540763.
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AAK53762 standard; cDNA; 278

AAK53762;

ВР.

(first entry) 16-NOV-2001

Murine transport and binding associated protein encoding cDNA SEQ ID 327. Murine; liver; gene library; amino acid synthesis; binding protein;

cell metabolism; energy metabolism; fatty acid metabolism; synthesis; phospholipid metabolism; purine; pyrimidine; nucleoside; nucleotide; replication; transport protein; ss.

Mus musculus

DE20103510-U1

28-FEB-2001; 2001DE-02003510

28-FEB-2001; 2001DE-02003510

(LION-) LION BIOSCIENCE AG

WPI; 2001-368570/39.

Gene library containing sequences with specific 3'-ends and no polyA tail, encoding proteins involved in a wide range of cellular processes.

Claim 15; Page 109; 251pp; German.

This invention describes a novel gene library (A) comprises a gene sequence (or its part) encoding a protein involved in amino acid synthesis, cellular/energy metabolism, metabolism of fatty acids/phospholipids, synthesis or breakdown of purines/pyrimidines/nucleosides/nucleotides, DNA replication/transcription/translation, or is a transport/binding protein. (A) are produced that correspond to the 3'-end of mRNA but without the polyA tail. They can be prepared more efficiently and with less effort than conventional libraries. AAKS1436-AAKS4275 represent fragments of the

Sequence 278 BP; 69 A; 72 C; 58 G; 79 T; 0 U; 0 Other;

library described in the method of the invention

1246 1306 ô CCAGGGAGGGGAGTCTATCTCCTCAAGTTTGATAATTCCTACTCTCTGTGGAGGTCCAAG 1366 TCCGTCTACTACAGAGTCTATTATACTAGATAGAGCTGCTGTTCCAAGGTCCGGAGTCCA 1426 218 158 86 1187 GAAAATGTCACTTGTGAAGAAAAAGCAAAAAAGAACGCCAACAAGCCTCTGCTGGATGAG GAAAATGTCACTTGTGAAGAAAAAGCAAAAAAGAACGCCAACAACAACAACCTCTGCTGGATGAG ccaedeaagagagactarcrccaagtrrcataarrccracrcrcrcracrecaega Gaps ö Length 278; Indels DB 4; Score 268.2; DB 4 Pred. No. 5.3e-62; 0; Mismatches 3 GGGTTGAGCACAACATGACGTTTAATTTCCTTT 1459 ഗ GGGTTGAGCACATGACGTTTAATTTCCTTT 18.4%; Query Match
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes 620499374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Suno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Suni, M., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matahiki, M., Ohazaki, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
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3433 bp mRNA linear HTC 03-APR-200 Mus musculus adult male pitutiary gland cDNA, RIKEN full-length enriched library, clone.5330404019, product:GOLGI RESIDENT PROTEIN GCF60 homolog [Homo sapiens], full insert sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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High-efficiency full-length cDNA cloning
Meth. Brzymol. 303, 19-44 (1999)
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the RIKEN Genome Exploration Research Group Phase II Team and the

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Functional annotation of a full-length mouse

FANTOM Consortium.

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Nature 409,

TITLE JOURNAL REFERENCE AUTHORS

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Result Š. m105h04.y AGENCOURT The FANTOM Consortium and the RIKEN Genome Exploration Research

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1056 TGGACAGGCCAAAACCCACACTGAAAATTCCGAAAAAGTCCTTGAGCCAGAAGCTGCAGA
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                                336 AATAAAAGGTGGCAAAGCCTTTCATCCAACTTATGAAGAAAAACTGAAGTTCGTGGCACT
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                                                                                                                Adachi, J., Aizawa, J., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.; Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramcto, K., Hiraoka, T., Hirozane, T., Hari, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsaco, N., Okazaki, Y., Saito, R., Satoh, H., Sakai, C., Sakai, K., Sakai, Sakai, K., Sakai, K., Sakai, K., Sakai, Sakai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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/dev_stage="adult"
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KREBEEKRRIE LEBELALLEOKOGINAALINSOTA VOPOVAAAOOY FORTSEO
LOEGHY QOYMOGLY VOVLAQOGAALOKOGEVWAAGASLPASSKWITAGASDTLSVNGO
AKTHTENSEKVLEPEAAEALENGPKOSLPY TAAPSMWITROLKOKTSOTANGO
AKTHTENSEKVLEPEAAEALENGPKOSLPY TAAPSMWITROLKOKTSOTA
TVRRGEVVITVR VPTHEEGS YLEWEFATIDS YD IGFGYY FEWTLS PNAAVSVHYSESSDE
EBEEDENINT CEEKAKKNANKPLLIDE I VPVYRRDCHEEVYAGSHOY FGRGYYLLKFDNS
YSLWRGKSVYTKVYTR?"
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YEEKLKFVALHKQVLLGPYNPDTSPEVGFFDVLGNDRRREWAALGNMSKEDAMVEFVK
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Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/.

URL:http://fantom.gsc.riken.jp/.

Location/Qualifiers.
                             functional annotation
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GCP60 homolog [Homo sapiens] (SPTR [09H3P7, evidence:
FASTY, 88.8%ID, 100%length, match=1575)
putative"
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Group Phase I & II Team.
Analysis of the mouse transcriptome based on of 60,70 tull-length cDNAs
Mature 420, 563-573 (2002)
6 (bases 1 to 3433)
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98.8%; Pred. No. 0;
iive 0; Mismatches
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/note="putative"
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Best Local Similarity 98.8
Matches 1347; Conservative
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AUTHORS
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                          TITLE
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QY 219 ATGTGTTGGGGAATGATAGGAGAATGGGCAGCTCTGGGAACCTCTCAGGAACCTGTCCAAGGAGG 78 Db 121 ATGTGTTGGGGAATGATAGGAGAGATGGGCAGCTCTGGGAAACCTGTCCAAGGAGG 180 QY 279 ATGCCATGGTAGAGTTGTGAACTTCTAAATAAGTGTTGTCCTCTCTCT	421 INDIANNIANIANIANIANIANIAGCAGCAGATAATGGCAGCTTTAAACTCGCAGACTGCCG 421 INDIANNIANIANIANIANIANIANIAGCAGCAGATAATGGCAGCTTTAAACTCGCAGACTGCCG 579 TGCAATTCCAGCAGTATGCAGCCCAGCAGTATCCAGGGAACTACGAACAACAGCAGATTC [759 CATTGCCTGCATCATCAAAGGTGAACACGTGAACCAAGTGATGCCTGCAGGTGATGCCTGCAGGTGATGCCTGCAGGTGAACCAGGTGAACCAGGTGAACCAGGTGAACCAGGTGAACCAGGTGAACCAGGTGAACCAGGTGAACCAGGTGAACCAGGTGAACCAGGTGAACCAGGTGAACCAGGTGAACCAGGTGAACCAGGTGAACCAGGTGAACCAGGTGAACCCAGAAAAGACTCCGAAAAAGTCCGTGAAAAAGACCAGAAAAGACTGCAAAAAGACCAGAAAAGACCAGAAAAGACCAGAAAAGACCTTGAAGCCAGAAGACTGCAGAAGACTTGCAAAAAGACCAAAAGAACTTCCAAAAAGACCTTGAAGACCCATCCAT		1119 CAGACTCTCCAAATGCTGTCAGTGTCAGTGAGTCAGTGAGTCAGTGAGGAGGAGG 178
	AY403085 LOCUS AY403085 LOCUS Mus musculus GOCAPI gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence. ACCESSION AY403085. AY40308	Perriera, S., Wang, G., Zhang, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M. Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios Science 302 (5652), 1960-1963 (2003) BD 14671302 CE 2 (bases 1 to 1301) CE 2 (bases 1 to 1301) CE 3 (bases 1 to 1301) CE 4 (bases 1 to 1301) CE 5 (bases 1 to 1301) CE 6 (bases 1 to 1301) CE 7 (bases 1 to 1301) CE 8 (bases 1 to 1301) CE 9 (bases 1 to 1301) CE 1 (bases 1 to 1301) CE 2 (bases 1 to 1301) CE 3 (bases 1 to 1301) CE 3 (bases 1 to 1301) CE 4 (bases 1 to 1301) CE 6 (bases 1 to 1301) CE 7 (bases 1 to 1301) CE 8 (bases 1 to 1301) CE 9 (base	COMMENT This sequence was made by sequencing genomic exons and ordering FEATURES Location/Qualifiers Source 1.1301 /organism="Mus musculus" /organism="Mus musculus" /db_xref="texon:10090" cl:>1301 /gene="GOCAP1" /locus_tag="HCM1439"	<pre>y Match Local Similarity 86.9%; Pred. No. 1.58-277; hes 1131; Conservative 0; Mismatches 170; Indels 0; Gaps 0; 99 TAAAAGATGGCAAAGCCTTCATCTTGAAGAAAACTGAAGTTCGTGGCACTGC 158 </pre>

Qy 277 GGATGCCATGGTAGATTTGTGAAGCTTCTAAATAAGTGTTGTCCTCTCCGCATA 33	Qy 396 AGCGAAGCCAGCTGAAGAGAACAGAGAGAAGAAGAAGAAGCGGA 455 Db 610 AGCGAAGCCGCTGAAGAAGAAGAAGAACGTCTGCAAAAGGAGAACGTA 669 Oy 456 AGCGAAGGCGGCTGAAGACGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG	DD 850 TTCTCATCCGCCAGTTGCAGGAGCAACACTATCAGCAGTACATGCAGCAGTTGTATCAAG 909	936 GGACAAGACCACAAATCAAAGACTTTAAAGAGAAGATTCGGCAGGATGCAGATTCTGTGA	1116 GGACAGACTCTCCAAATGCTGCTGTGCATGTCAGTGAGTCCAGTGAGTCCAGTGAGGAGG 1171
1357 GAGGTCCAAGTCCGTCTACTACTATTATACTAGATAGAGCTGCTGTTCCAAGGT 1416	RESULT 4 BC039575 BC039575 BC039575 BC039575 BC039575 BC039575 HOMO sapiens, clone IMAGE:5725757, mRNA. BC039575 BC03957 BC039575 BC03957 B	USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: Invitrogen CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Innstitute for Systems Biology DNA Sequencing by: Innstitute for Systems Biology http://www.systemsbiology.org contact: amadan@systemsbiology.org Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting Clome distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILL at: http://image.llnl.gov Series: IRAK Plate: 84 Row: Column: 21 This clone was selected for full length sequencing because it	passed the following selection criteria: matched mRNA gi: 15826851 This clone has the following problem: retained intron. Location/Qualifiers 1. 1995 Aorganism="Homo sapiens" Ab xref="Homo sapiens" Ab xref="taxon:9506" /clone="WAGE:572572" /tissue type="Wary, pooled from 3 adults" /clone="Type="Wary, pooled" /lab host="DH10B" /note="Vector: pCMV-SPORT6"	Query Match 73.2%; Score 1068.6; DB 3; Length 1995; Best Local Similarity 87.1%; Pred. No. 3.7e-263; 1 Matches 1184; Conservative 0; Mismatches 174; Indels 1; 97 AGTAAAAGATGGCAAAGCCTTTCATCCAACTTATGAAGAAAAATTGAAGCTTGTGGACT 156 111111111111111111111111111111111111

400 AAGGCAGCGTGAAGAAGAACGAGAGCGGCTGCAAAAGGAAGAAGAGAAGCGGAAGCG 459 302 NYNNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYN	NINDINININININININININININININININININI	Db 1082 GGAAGAAGAAAACATGGTAGGAAGAAGAAGAAGAAGAAGAAGAAGACCTTGGT 1141 1082 GGAAGAAGAAAAACATGGTTGTAGAAGAAAGAAGAAGAAGAAGAACAACAAGAAGAAGAAGA
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962 CTTTTGGGAATTTGCCACAGACAATTATGACATTGGGGTTTGGGGTGTATTTTGAATGGCA 1021
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BY757076 RIKEN full-length enriched, blastocyst Mus musculus cDNA
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Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 726)
Mokazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
                          CATCCGCCAGCTGCAGGAGCAGCACTATCAGCAGTATAAACACCAGGCAGAGCAAACCCA
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        GCAATTCCAGCAGTATGCAGCCCAGCAGTATCCAGGGAACTACGAACAACAGCAGATTCT
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Forfier, A.G., Clanowski, S., Wangh, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
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Direct Submitsed on Cargill, M.
Borkettle, (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Best Local Similarity 76.4%; Pred. No. 3e-224;
Matches 992; Conservative 0; Mismatches 307; Indels
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/mol_type="genomic DNA"
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Science 302 (5652), 1960-1963 (2003)
14671302
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/locus_tag="HCM1439"
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                                                                  Pan troglodytes (chimpanzee)
Pan troglodytes
genomic survey sequence
AY403084
AY403084.1 GI:39759067
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organism="Mus musculus"
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B84 bp mRNA linear EST 03-SEP-2002
AGENCOURT_7938530 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6012409
BU153320
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1. (bases 1 to 884)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                Length 726;
                                                                                                                                                                           GCTGAGACGGGAGGAGGAGGAGGCGGCGGATAGAGGAAGAGAGGCT
                                                                                                             Indels
                                                                                                             19;
                                                DB 6;
                                          Score 686.6; DB 6;
Pred. No. 4.2e-165;
0; Mismatches 19;
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                                          Query Match
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Matches 706; Conservative
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Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalo, S., Bislea, K.W., Blake, J.A., Bardi, D., Brusic, V., Chothia, C., Corbani, L.E., Cousine, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Garibodid, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Kanodrincich, S., Hirokawa, N., Jackson, I.J., Jarvis, B.D., Kanai, A., Kuvochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Perchards, N., Partiais, R., Pontius, J.U., Qil, D., Ranachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M., S., Yang, L., Wanger, L., Wahlestedt, C., Wang, Y., Waragisawa, M., Yang, L., Yang, L., Yang, L., Wahlestedt, C., Wang, Y., Waragisawa, M., Yang, L., Wahlestedt, C., Wang, Y., Marakawa, T., Pukuda, S., Hara, A., Hashizume, M., Tawa, K., Itch, M., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, B. and Hayashizaki, Y. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Genome Genomic Sciences Center and Genome Science Laboratory in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email genome_rese@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Rukuda,S., Hashizume,M., Hayashida,K., Hirozane,T., Hori,F.,
Imoteni,K., Ishii,Y., Itch,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo;S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohasto,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Direct Submission
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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/strain="C57BL/6J"
/bb_xref="taxon:10090"
/clone="11C0048M22"
/dev stage="blastocyst"
/clone_lib="RIKEN full-length enriched, blastocyst"
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1134

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Sharov, A.A., Piaco, Y., Matoba, R., Dudekula, D.B., Qian, Y., VanBuren, V., Falco, G., Martin, P.R., Stagg, C.A., Bassey, U.C., WanBuren, V., Falco, G., Martin, P.R., Stagg, C.A., Bassey, U.C., Wang, Y., Carter, M.G., Hamatani, T., Aiba, K., Akutsu, H., Sharova, L., Tanaka, T.S., Kimber, W.L., Yoshikawa, T., Jaradat, S.A., Pantano, S., Nagaraja, R., Boheler, W.R., Taub, D., Hodes, R.J., Longo, D.L., Schlessinger, D., Keller, J., Klotz, E., Kelso, G., Umczawa, A., Vescovi, A.L., Rossant, J., Kunath, T., Hogan, B.L., Curci, A., D'Urso, M., Kelso, J., Hide, W. and Ko, M.S.

Transcriptome analysis of mouse stem cells and early embryos ploss stem calls and early embryos ploss stem contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Sulte 4000, Baltimore, MD 21224-6820, USA Email: cdns@lgsun.grc.nia.nih.gov
Plate: E0463 row: B column: 05
Seq primer: M13 Reverse
High quality sequence stop: 653
                                                                                                                                                                                                                                                            1184 GAAGAAAATGTCACTTGTGAAGAAAAAAAAAAAAAAGACGCCAACCACCTCTGCTGGAT 1243
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                                                                                                                                                                                                                                                                                                                                                                                                             EST 18-MAY-2004
                                                                                                                                                                   GAAGANAACATCGGTTGTGAAGAAAGAAAGAATGGCAACAAGACTTTGCTGGAT 781
           CN702497 18-MAY-200
653 bp mRNA linear EST 18-MAY-200
653 bp mANOLE embryo cDNA library (Long) Mus
musculus cDNA clone NIA:E0463B05 IMAGE:30874576 5', mRNA sequence.
CN702497
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 653)
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/db_xref="niablou"
/db_xref="taxon:10090"
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/tissue="type="whole embryo including extraembryonic tissues at 11.5-days postcoitum"
/dev stage="E11.5"
/lab_host="bH108"
/clone lib="NIA Mouse E11.5 whole embryo cDNA library /clone)"
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/strain="C57BL/6J"
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Mus musculus
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                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information clone distribution: MGC clone distribution information clone through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM1303 row: k column: 02
High quality sequence stop: 645.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone=IMAGE:6012409"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH108 [phage-resistant)"
/clone lib="NH1M MGC 92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
Unpublished (1999)
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Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

EST. Mus musculus (house mouse)

Mus musculus Eukaryota; Metazoa; C Mammalia; Eutheria; R 1 (bases 1 to 653)

GI:34586303

CF534335.1

NIH-MGC http://mgc,nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. Jim Lin, University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

 .653 /organism="Mus musculus"

Location/Qualifiers

Seg primer: pYX-5.

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VERSION
KEYWORDS
SOURCE
ORGANISM
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TITLE
JOURNAL
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postcoitum. Double-stranded cDNAs were synthesized with an Oligo (dT) primer [Invitrogen:
5'-pGACTAGTTCTAGATCGCGACGCCCCTTTTTTTTTTTTT3'] from
2ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to Lone-linker LL-Sal4, purified by phenol/Chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Tag polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with Sal1 and NoI enzymes
and cloned into Sal1/Not1 site of pCNV-SPORT6 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by the standard chemical method. The
average insert size is about 3.3Kb. The library was
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Pred. No. 5.8e-152;
0; Mismatches 11;
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/tissue_type="whole brain"
/dev stage="whole brain"
/dev stage="whole brain"
/dev stage="whole (TI phage resistant)"
/clone lib="NIH BMAP FYO"
/clone lib="NIH BMAP FYO"
/clone lib="NIH BMAP FYO"
/site="Organ: Brain; Vector: pYX- Asc; Site=1: EcoR I;
Site=2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel: First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not! and then cloned
directionally into pYX-Age vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     695 ACCCAACCTGCACAACAACAGGCAGCATTACAGAAAACAGCAAGAAGTAGTGGTGGCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           755 GCATCATTGCCTGCATCATCAAAGGTGAACACAGCTGGAGCAAGTGATACACTGTCAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGAGGCTTCGGCTGGAACAGCAAAAGCAGCAGATAATGGCAGCTTTAAACTCGCAGACT
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Pred. No. 2.7e-151;
0; Mismatches 13;
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30363791"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  program coordinator."
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Best Local Similarity 98.0%;
Matches 640; Conservative
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CF534335
UI-M-FYO-CGT-b-24-0-UI.x1 NIH BMAP_FYO Mus musculus cDNA clone
IMAGE:30363791 5', mRNA sequence.
CF534335

RESULT 10 CFS34335 LOCUS DEFINITION

ACCESSION

resulted in an average insert size of 2.2 kb. This prim library is normalized (non-normalized primary library is normalized (non-normalized primary library in the More of Sister of Siste	62 ACAGCTGGAGCAGCTGCTGCCCTGCCAGTGGACGGACCGAGACCCACACTGAGAAT 845 TCCGAAAAAGTCCTTGAGCCAGAAGCTGCAGAAGACCCTTGGAAAATGGACCAAAAGAC 122 CCCGAGAAAAGTCCTTGAGCCAGAAGCTGCGGAAAGAGCCTTGGAAAATGGACCCAAAGAC 905 TCTCTTCCAGTGATTGCAGCTCCATCCATGTGGACAAAGACCTTAAA 182 TCTCTTCCAGTGATTGCAGCTCCATCCATGTGGACAAAGACCACAAAGACTTTAAA 965 GAGAAGATTGGAGTGCTCCTTCCATGTGATTACAGTACGTGAGAAGACCTTTAAA 965 GAGAAGATTGGGGATGCAGATCTGTGATTACAGTACGTCGAGGAGAAAGACCTTTAAA 967 GAGAAGATTCGGCAGGATCCATGTGATTACAGTACGTCGAGGAGAAAGTCGTCACCCTTTTAAA 968 GAGAAGATTCGGCAGGATCTGTGATTACAGTACGTCGAGGAGAAAGTCGTCACCCTTTTAAA 968 GAGAAGATTCGGCAGGATCTGTGATTACAGTACGTCGAGGAGAAAGTCGTCACCTTTTAAA 11	Db 242 GAGAAGATTCGGCAGGATTCTGTGATTACAGTCCGGCGAGGAGAAGTAGTCACC 301 Qy 1025 GTCCGAGTCCGACTCATGAGGAAGGATCATATTGGCAATTTCCCACAGAGAGT 1084 302 GTTCGAGTCCCCACTCATGAGGAAGGATCATTTGGGAATTTGCCACAGACAG	Qy 1262 GAAGAAAAAGCAAAAAGCCCAACAAGCCTCTGCTGGATGAGTTGTACCTGTGTAC 1261 Bb 482 GAAGAGAAAAGAATGTCAACAAGCCTCTGCTGGATGAGTTGTACCTGTGTAC 541 Qy 1262 GGGGGGACTGTCACGAGAAGTATATGCAGCCACCAGTATCCTGGGAGGGGGTC 1321 Db 542 CGGCGGACTGTCACGAGAAGTATATGCAGCCACCAGTACCTGGGAGGGGGTC 601 Qy 1322 TATCTCCTCAAGTTGAAAATCCTTCTGTGGAGGTCCAAGTCCATACAGA 601 Db 602 TATCTCCTCAAGTTGATAACTCCTTCTGTGGAGGTCTAAGTCAGTC	Qy 1442 TGACGTTTAATTTCCTT 1458
	00 0055 TACCTATTTGCGGAATTTGCCACAGACGGTTAGGGGTTTGGGGTTTTGAA 1114	AGENCOURT 17895630 NIH MGC 234 Rattus norvegicus cDNA clo RAGENCOURT 17895630 NIH MGC 234 Rattus norvegicus cDNA clo CK600219	Contract: Daniela S. Gerhard, Ph.D. Contract: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bidg. 31 Rm10A07 Bethesda, MD 20892 Email: cgapbs-r@mail.nih.gov Tissue Procurement: Howard Jacobs CDNA Library Preparation: Express Genomics CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) MN Sequencing by: Ageniciant Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAMI5046 row: b column: 09 High quality sequence stop: 695.	

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/db xref="taxon:1090"
/db xref="taxon:1090"
/clone="ip04a04"
/tlsue_rype="whole eye"
/dev stage="Adult"
/lab_host="EMDH10B"
/lab_host="EMDH10B"
/lab_host="EMDH10B"
/clone lib="Mouse Whole eye, unamplified: io/ip"
/lote="Grgan: Eye, Vector: pSport1; Approximately Img
/note="Grgan: Eye, Vector: pSport1; Approximately Img
/ctal RNA was extracted from 200 adult mouse whole eyes. A
directionally cloned cDNA library in the pSPORT1 vector
(Invitrogen) was constructed at Bloserve Biotechnology
(Laurel MD) essentially following the protocols of the
Superscript Plasmid System full details of which are
contained in the manufacturer's Instruction manual
(http://www.lifetech.com/). First strand synthesis was
carried out using a Not I primer-adapter
[5'-pGACTAGTTCTAGATCGCGGGGGGCGCCC(T)]5-3']. cDNA was
cloned in Not I/Sal I sites. EST analysis was performed on
the unamplified library at the NIH Intramural Sequencing
                                                                                                                                                                                                                                                                                                                                                             CK627880 603 bp mRNA linear EST 26-JAN-2004 ip04a04.yl Mouse Whole eye, unamplified: io/ip Mus musculus cDNA clone ip04a04.y, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
Mus musculus
Mus musculus
Mus musculus
Musia, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Musicu, G.

1 (bases 1 to 603)
Wistow, G. and Tomarev, S.
Wistow, G. and Tomarev, G.
Unpublished (2004)
                              526 CACCAGTATCCA-GGAGGGAGTCTATCTCCTCAAG-TTGATAATTCCTACTCTCTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GTTGCGTCCCACAGAATAGAAGAAGAAGAAGAAGAAGAAAAGAAGAAGAGGGGAGGAGGAG
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                                                                                                                                                                                                    1418 CGGAGTCCAGGG-TTGAGCACACATGACGTTTAATTTCCTTT 1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 585.4; DB 7; Length Pred. No. 4e-139; 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                  989
                                                                                                                                                                                                                             644 GGGAGTCTAGGGTTTGAGCACAACATGACGTTTAATTTCCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: graeme@helix.nih.gov
Plate: 04 row: a column: 04
Seq primer: M13RPL reverse primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57816J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CK627880.1 GI:41348766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.1%;
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Best Local Similarity 98.2<sup>3</sup>
Matches 592; Conservative
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                         RESULT 13
CK627880
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
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                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
thtp://image.llnl.gov. k column: 08
High quality sequence stop: 680.
Location/Qualifiers
Location/Qualifiers

i. 757
/ organism="Mus musculus"
/ mail type="markN"
/ db xref="taxkn"
/ lab_host="taxkn"
/ lab_host="DH108 (phage-resistant)"
/ lab_host="DH108 (phage-resistant)"
/ loone lib="NHH MGC 94"
/ note="Organ: eye; Vector: pCNV-SPORT6; Site_I: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dfr primed.
Average insert size 3.3 &b. Library enriched for
Average insert size 3.3 &b. Library enriched for
Average insert size 3.3 &b. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1118 ACAGACTCTCCAAATGCTGCTGTCAGTGTGCATGTCAGTGAGTCCAGTGAGGAGGAG
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  Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
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                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
1 (bases 1 to 757)
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Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st srand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and Ecox V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
CGAGAGGAGGAAGCCGCTGAGACGGGAGGAGAGAGAGAGGCGGCGGATAGAGGAAGAG
                                                                                                                                      TCATTGCCTGCATCATCAAAGGTGAACACAGCTGGAGCAAGTGATACACTGTCAGTTAAT
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                                                                                                      AGGCTTCGGCTGGGACAGCAGCAGCAGATAATGGCAGCTTTAAACTCGCAGACTGCC
                                                                                                                            GTGCAATTCCAGCAGTATGCAGCCCAGCAGTATCCAGGGAACTACGAACAACAACAGCAGATT
                                                                                                                                                                       CTCATCCGCCAGCTGCAGGAGCACCACTATCAGCAGTATAAACACCCAGGCAGAGCAAACC
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Unpublished (2001)
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Homo sapiens (human)
Homo sapiens
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/clone=lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="list strand cDNA was primed with a NotI-oligo(dT)
primer Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                                                                                                                                                                                39.5%; Score 576.6; DB 1;
83.2%; Pred. No. 8.9e-137;
ive 12; Mismatches 118;
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/organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxnA"
/tissue_type="embryonic stem cells, embryoid bodies
/tissue_type="embryonic stem cells"
/tissue_type="embryonic stem cells"
/clone_lib="graw lB"
/note="oligo dT primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
fil (p22), #7 (p29), and H9 (p26) maintained in feeder-free
conditions."
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1700044186898 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
CN310226
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Tel: 650 473 8658
Fax: 650 473 7760
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                                                                                                                                                                                                                                                                                                                                                                                                Email: rbrandenberger@geron.com
Insert Length: 792 Std Error: 0.00.
Location/Qualifiers
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Homo sapiens
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AC013513 Drosophil
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AC12129 Mus muscu
AJ720156 Gallus ga
AK40067 Sequence
AY598329 Homo sapi
AK833708 Sequence
AK09556 Homo sapi
AC140763 Rattus no
AC126290 Rattus no
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Mus musculus peripherial benzodiazepine receptor associated protein
(Papy) mRNA, complete cds.
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ACC44825 Homo sapi
ACC31883 Homo sapi
BCC54676 Danio rer
BX510322 Zebrafish
Z95559 Caenorhabdi
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Li, H., Degenhardt, B., Tobin, D., Yao, Z.X., Tasken, K. and Papadopoulos, V.
Identification, localization, and function in steroidogenesis of PAP7: a peripheral-type benzodiazepine receptor- and PKA (Rialpha)-associated protein (Rialpha)-associated (Rialpha)-
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Gallus ga
Sus scrof
Homo sapi
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Mus musculus
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Li,H. and Papadopoulos,V.
Direct Submission
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-0=(GgD2 1/05PTO gpool/USO9762594/runat 19082005_171348_18319/app_query.fasta_1.647
-0=(GgD2 1/05PTO gpool/USO9762594/runat 19082005_171348_18319/app_query.fasta_1.647
-0=GGDIEMD1-OFWT=fastap -SUFFTX=rge -MINWATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-0-OALIGN=200 -THR SCORE=CT -THR MIN=10 -ALIGN=15 -MODE=LOCAL
-OUTPMT=ptc -NORM=ext -HBAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=USO9762594_@CGN_1_1_3731_@runat_19082005_171348_18319 -NCPU=6 -ICPU=3
-NO MAAP -LARGEQÜERS -NGG SCORES=0 -WAIT -DSPEDCCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -SGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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BC060602 Mus muscu
AY336075 Rattus no
BC083877 Rattus no
                                                                                                                           August 23, 2005, 00:08:19; Search time 6200 Seconds (without alignments) 3618.510 Million cell updates/sec
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                         - nucleic search, using frame_plus_p2n model
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Kgapop 10.0 , Kgapext 0.5
Kgapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop, 6.0 , Delext 7.0
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1: gb_ba:*

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                                                                                                                                                                                                                                                      LeulleArgGlnLeuGlnGluGlnHisTyrGlnGlnTyrLysHisGlnAlaGluGlnThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1537 CACCAGTATCCAGGGAGGGGAGTCTATCTCCTCAAGTTTGATAATTCCTACTCTGTGG
ArgleuArgleuGluGlnGlnLysGlnGlnIleMetAlaAlaLeuAsnSerGlnThrAla
                                                                                                                                           AGGCTTCGGCTGGAAACAGCAAAAAGCAGATAAATGGCAGCTTTAAACTCGCAGACTGCC
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                                                   ArgGluGluAspArgLeuArgArgGluGluGluGluArgArgIleGluGluGlu
                                                                                                                                                                                                             GTGCAATTCCAGCAGTATGCAGCCCAGCAGTATCCAGGAACTACGAACAACAGCAGATT
                                                                                                                                                                                                                                                                                                                      GlnProAlaGlnGlnGlnAlaAlaLeuGlnLysGlnGluValValValMetAlaGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                        271 GlyGlnAlaLysThrHisThrGluAsnSerGluLysValLeuGluProGluAlaAlaGlu
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                                                                                                              Li, H., Liu, J. and Papadopoulos, V.

Li, H., Liu, J. and Papadopoulos, V.

Direct Submission
Submitted (13-SEP-2002) Department of Cell Biology, Georgetown
University Medical Center, 3900 Reservoir Rd. NW, Washington, DC
20007, USA
Sequence update by submitter
On Sep 13, 2002 this sequence version replaced gi:7545290.
   Li,H. and Papadopoulos,V.
Direct Submission
Submitted (12-APR-2000) Department of Cell Biology, Georgetown
University Medical Center, 3900 Reservoir Rd. NW, Washington, DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATAAAAAGATGGCAAAAGCCTTTCATCCAACTTATGAAGAAAAACTGAAGTTCGTGGGACTG
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                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs.remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
Thomas L. Casavant.
Thomas L. Casavant.
Web site: http://genome.uiowa.edu
COntact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
COntact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu.I., Bair,T., Bair,J., Crouch,K., Davis,A.,
Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at: http://image.llnl.gov Series: Plate: Row: Column: 0. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (31-OCT-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Acbd3"
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                                                              Mus musculus
    VERSION
KEYWORDS
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ORGANISM
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AUTHORS
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Sciurognathi, Muridae, Murinae,
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                                  GlyGlnAlaLysThrHisThrGluAsnSerGluLysValLeuGluProGluAlaAlaGlu
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Center, 1501 Kings Highway, Shreveport, LA 71105, USA
Location/Qualifiers
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Chen, Y., Rodriguez-Paris, J.M., Ma, Y., Yeh, M., Yeh, K.-Y. and
Glass, J.
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Iron Responsive Protein
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Chen,Y., Rodriguez-Paris,J.M., Ma,Y.,
Glass,J.
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Rattum norvegicus DMT1-associated
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Mammalia; Eutheria; Rodentia;
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Rattus norvegicus
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WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Bmail: capabbs-remail.nih.gov
Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 184 Row: h Column: 2
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 33469058.
Location/Qualifiers
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Jockson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                         2 (bases 1 to 1927)
Director MGC Project.
Direct Submission
Submitted (01-0CT-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
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Conservative:
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Best Local Similarity:
Query Match:
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Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Morce, T., Max, S.I., Wang, J., Haich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, W.M. B., Bonaldo, M.F., Casavant, T.L.,
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Rattus norvegicus DMT1-associated protein, mRNA (cDNA clone
MGC:95164 IMAGE:7130229), complete cds.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                            SerLeuProAlaSerSerLysValAsnThrAlaGlyAlaSerAspThrLeuSerValAsn
                                                            995 rchridecridecranananderdandanderdandrangerdanderdecendrander
                                                                                                        GlyGlnAlaLysThrHisThrGluAsnSerGluLysValLeuGluProGluAlaAlaGlu
                                                                                                                                                GGACAGGCCAAGACCCACACTGAGAATCCCGAAAAAGTCCTTGAGCCAGAAGCTGCGGAA
                                                                                                                                                                                                                                                                                       ThrArgProGlnIleLysAspPheLysGluLysIleArgGlnAspAlaAspSerValIle
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SDDDEBEBERNIGGERKAKRNNKPLLDEIVPVYRRCHEBEVYAGSHQYPGRGYYLLKF
DNSYSLWRSKSVYYRVYTR"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [bases 1 to 3598]
Misumi, Y., Ikehara, Y. and Sohda, M.
Discut Submission
Submitted (23-MAY-2000) Yoshio Misumi, Fukuoka University School
Bedicine, Depertment of Biochemistry; 45-1, 7 chome Nanakuma,
Jona-ku, Fukuoka, Fukuoka 814-0180, Japan
(B-mail:misumi@fukuoka-u.ac.jp, Tel:81-92-801-1011(ex.3251),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identification and characterization of a novel Golgi protein, GCP60, that interacts with the integral membrane protein giantin J. Biol. Chem. 276 (48), 45298-45306 (2001)
1496 AGCCACCAGTACCCAGGGAGGGGGTCTATCTCTCAAGTTTGATAACTCCTACTCTG
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                                                                                                                         LeuLeuAspGluIleValProValTyrArgArgAspCysHisGluGluValTyrAlaGly
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On Sep 27, 2001 this sequence version replaced gi:12060408.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sohda,M., Misumi,Y., Yamamoto,A., Yano,A., Nakamura,N. and
Ikehara,Y.
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for golgi resident
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1016 GGACAGGCCAAGACCCACACTGAGAATCCCGAGAAAGTCCTTGAGCCAGAAGCTGCGGAA 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1076 GAGGCCTTGGAAAATGGACCCAAAGACTCTCTCCAGTGATTGCAGCTCCTTCCATGTGG 1135
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                                                                                                                                                                                                                                                416 GATGTTTGGGGAATGATAGGAGGAGAGAATGGCCAGCTCTGGGAAACATGTCCAAAGAG 475
                                                                                                                                                                                                                                                                                                                                                                                                                             ArgArgGlnArgGluGluGluArgGluArgLeuGlnLysGluGluGluLysArgLys 150
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                                 x BC083877 (1-1927)
                                  US-09-762-594-7 (1-463)
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332 ValArgArgGlyGluValValThrValArgValProThrHisGluGluGlySerTyrLeu	1244 GTGGGCCGAGGAGAGTCGTCGAGTACCCACCCATGAAGAAGGATCATATCTC 352 PheTrpGluPheAlaThrAspSerTyrAspIleGlyPheGlyValTyrPheGluTrpThr 1304 TTTTGGGAATTTGCCACAGACAATTATGACATTGGGGTTTGGGGTGTTTTGAATGGACA 372 AspSerProAsnAlaAlaValSerValHisValSerGluSerSerAspGluGluGluGluGlu	DD 1364 GACICICCAAACACTGICAGCGIGCAIGTCAGTGAGTCCAGCGATGACGACGAGGAG 1423 Qy 392 GluGluGluAsnValThrCysGluGluLysAlaLysLysAsnAlaAsnLysProLeuLeu 411	Qy 412 AspCluIleValProValTyrArgArgAspCysHisGluCluValTyrAlaClySerHis 431 Db 1484 GATGAGATTGTGCCTGTGTACCGACGGACTGTCATGAGGACGTGTATGCTGCAGCAGTT 1543	Oy 432 GlnTyrProGlyValTyrLeuLeuLy8PheAspasnSerTyrSerLeuTrpArg 451	Oy 452 SerlysSerValTyrTyrArgValTyrTyrThrArg 463 	RESULT 6 AK025520 AK025520 AK025520 AK025520 DEFINITION Homo sapiens CDNA: FLJ21867 fis, clone HEP02419.	AK025520 AK025520.1 GI:10438060 Oligo capping; fis (full insert E Homo sapiens (human)	Σ			TITLE Direct Submitsaton JOURNAL SUbmitted (19-AUG-2000) Sumic Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,	Japan (E-mail:flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416) COMMENT NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert	<pre>sequencing: Research Association for Biotechnology; cDNA library construction, S'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology</pre>	Agency). FEATURES Location/Qualifiers Source 12140 /organism="Homo sapiens"	/mol_type="mkNA" /db_xref="texon:9606" /clone="HEP02419" /cell_line="HepG2"	/cell_type="hepatoma" /clone_lib="HEP" /note="cloning vector pME18SFL3" CDS 491635
3'UTR 1643.3580 ORIGIN /gene="gcp60"	Alignment Scores: Pred. No.: 2046.00 Matches: Score: Score: 9.014 Length: 3598 Score: 9.028* Matches: 20 Best. Local Similarity: 90.28* Mismatches: 22 Query Match: 95.46* Indels: 0 DB:	-09-762-594-7 (1-463) x AB043587 (1-3598) 32 LygAspGlyLysAlaPheHisProThrTyrGluGluLygLeuLysPheValAlaLeuHis	DD 544 AMGAIOCLAAACLIIICAICCAACIIAIGAAGAAAATIGAAGCIIGIGGGACIGCAI 403 QY 52 LygGlnValLeuLeuGlyProTyrAsnProAspThrSerProGluValGlyPhePheAsp 71 DD 404 AAGCAAGTICTTAIGGGCCATATAATCCAGAAGTTTGTTCCTGAGAGTTTGTTATAATAA 443	72 ValleuGlyAsnAspArgArgGluTrpAlaAlaLeuGlyAsnMetSerLysGluAsp 	Oy 92 AlaMetValGluPheValLysLeuLeuAsnLysCysCysProLeuLeuSerAlaTyrVal 111	Qy 112 AlaSerHisArgIleGluLysGluGluGluUluLysArgArgLysAlaGluGluArg 131	Oy 132 ArgGlnArgGluGluGluGluArgGluArgLeuGlnLysGluGluGlysArgLysArg 151 :::	Qy 152 GluGluBupargLeuArgArgGluGluGluGluArgArgArgIleGluGluGluArg 171 Db 704 GAAGAAGGAAGGAAAGGGAGGAAGAGAAGAGAAGAGA	Qy 172 LeuArgLeuGluGlnGlnLysGlnGlnIleMetAlaAlaLeuAsnSerGlnThralaVal 191 Db 764 CTTCGGTTGGAGCAGCAAAAGCAGCAGATAATGGCAGCTTTAAACTCCCAGACTGCCGTG 823	Qy 192 GlnPheGlnGlnTyrAlaAlaGlnGlnTyrProGlyAsnTyrGluGlnGlnGlnGlnIleLeu 211 Db 824 CAGTTCCAGCAGTATGCAGCCCAACAGTATCCAGGGAACTACGAACAGCAGCAACTTCTC 883	Oy 212 IleArgGInLeuGlnGluGlnHisTyrClnGlnTyrLysHisGlnAlaGluGlnThrGln 231 Db	Qy 232 ProAlaGlnGlnAlaAlaLeuGlnLysGlnGlnGlnValValMetAlaGlyAlaSer 251 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 252 LeuProAlaSerELysValAsnThrAlaGlyAlaSerAspThrLeuSerValAsnGly 271	Oy 272 GlnAlaLysThrHisThrGluAsnSerGluLysValLeuGluProGluAlaAlaGluGlu 291	Oy 292 AlaLeuGluAsnGlyProLysAspSerLeuDroVallleAlaAlaProSerMetTrpThr 311	Oy 312 ArgProGlnIleLysAspPheLysGluLysIleArgGlnAspAlaAspSerValIleThr 331

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Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 3358)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausberg, R.L., Reingold, E.A., Grouse, L.H., Derge, J.G.,
Klausberg, R.L., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhar, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S. I., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Sahutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Sahutz, J., Myers, R.M.,
Generation and initial analysis of more than 15,000 full-length
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                  GlnAlaLysThrHisThrGluAsnSerGluLysValLeuGluProGluAlaAlaGluGlu
                                                                                               AlaLeuGluAsnGlyProLysAspSerLeuProVallleAlaAlaProSerMetTrpThr
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| Da.xreE="GI:10438061"
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                                                                                                             HPTYEEKLKI.VALHKOVIMGPYNPDTCPEVGFPOVIGNDRRREWAALGNMSKEDAMVE
FVKLINRCCHLFSTYVASHKI EKEEQDKKRKEEEERRRREEEERRLQKEEEKRREE
EERLRREEEERRRI EEERLRLEQQKQQIMAALNSQTAVQFQQYAAQQYPGNYEQQQII
                                                                                                                                                                       IRQLOEQHYQQYMQQLYQVQLAQQQAALQKQQEVVYAGSSIPTSSKVNATVPSNNMSV
QQAXTHTDSSEKELEPPEABELENGPRESLEVIAAPEMNTRPQIRDKFEKILQDDAD
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SDDDEEBEENIGCEEKAKKNANKPLLDEIVPVYRRDCHEEVYAGSHQYPGRGVYLKF
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/note="unnamed protein product"
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100-762-594-7 (1-463) x BC060792 (1-3358)	52 392 72 452 92 512	572 GCGTCCCACAAATAGAGAAGAAAAAAAAAAAAAAAGGAAGG	y 192 GlnPheGlnGlnTyrAlaAlaGlnGlnTyrProGlyAsnTyrGluGlnGlnGlnIleLeu 211 812 CAGTTCCAGCAGTATGCAGCCCAACAGTATCCAGGGAACTACGAACAGCAGCAAATTCTC 871 212 IleArgGlnLeuGlnGluGlnHisTyrGlnGlnTyrLysHisGlnAlaGluGlnThrGln 231 872 ATCCGCCAGTTGCAGGACCAACACTATCAGCAGTACATGCAGCAGTTGTATCAAGTCCAG 931 7 232 ProAlaGlnGlnGlnAlaAlaLeuGlnLysGlnGlnGluValValWetAlaGlyAlaSer 251 873 CTTGCACAGCAAGGCAGCAGTATCAGAAAGTAGTGCAGGGTTCTTATCAGGTTCTTATCAGTAGTGCAGGTTCTTATCAGGTTCTTATCAGGTTCTTATCAGGTTCTTATCAGGTTCTTATCAGGTTCTTATCAGGTTCTTATCAGGTTCTTATCAGGTTCTTATCAGGTTCTTATCAGGAAGTTCTTATCAGGAACTTTATCAGAAACAAGGAAGTTGTTATCAGAAACTAGTTGCTTCT 991	252 LeuprohlaSerSerLyeVallanThralaGlyAlaSerAspThrLeuSerVallanGly [] [] [] [] [] [] [] [] [] [] [] [] []
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human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 12477932 2 (bases 1 to 3358) Strausberg, R. Direct Submission Submitted (03-NOV-2003) National Institutes of Health, Mammalian Gene Collection (WGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,	USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbe-r@mail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.	Clone distribution: MGC clone distribution information can be found through the 1.M.A.G.E. Consortium/Linn at: http://image.llnl.gov Series: IRAK Plate: 133 Row: 1 Column: 24 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 15826851. Location/Qualifiers 1.3358 /organism="Homo sapiens" /mol_type="mRNA" /mol_type="mRNA" /doc=mRNA" /clone="MGC:11593 IMAGE:4813993" /tissue_type="Brain, hdippocampus"	/clone llb=MNH MGC_95" /lab_host="MH10B" /note="Vector: pBluescript" .358 /gene="ACBD3" /mote="Bynonyms: GCP60, PAP7, GOCAP1, GOLPH1" /db_xref="LocusID:64746" /db_xref="LocusID:64746" /db_xref="MH:606809" /411630 /gene="ACBD3" /codon_start=1 /product="ACBD3 protein"	E E B B B B B B B B B B B B B B B B B B
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Qy 392 GluGluAsnValThrCysGluGluLysBlaLysBAshAlaAsnLysProLeuLeu 411	ଧ ଶ	72 ValleuGlyAsnAspArgArgArgGluTrpAlaAlaLeuGlyAsnMetSerLy8GluAsp 9
Oy 412 AspGluIleValProValTyrArgAspCysHisGluGluValTyrAlaGlySerHis 431 	à a	92 AlaMetValGluPheValLysLeuLeuAsnLysCysCysProLeuLeuSerAlaTyrVal 1
432 GlnfyrbroGlyArgGlyValTyrLeuLeuLy8PheAspAsnSerTyrSerLeuTrpArg 4	<i>≿</i> a	alaserhisargilegiulysgiuglugiugiulysargarglysalagiuglugiularg
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ue,H., Corley,N.C., Guegler,K.J erson,C. ssociated proteins	& g	212 IleargGlnLeuGlnGluGlnHisTyrGlnGlnTyrLysHisGlnAlaGluGlnThrGln 2
	čo qa	232 ProAlaGInGInGInAlaAlaLeuGInLysGInGInGIuValValMetAlaGIyAlaSer 2
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ers	\$ g	292 AlaLeuGluAsnGlyProLysAspSerLeuProVall1eAlaAlaProSerMetTrpThr 3
	\$ £	312 ArgFroGlnIleLysAspPheLysGluLysIleArgGlnAspAlaAspSerValIleThr 3
/ Ab_rref="taxon:9606" / Ab_rref="taxon:9606"	? <i>&</i>	
4.17e-143 Length: 2021.00 Matches:	ବ ଧ	
Conservative: 22 Best Local Similarity: 89.12% Mismatches: 25 Query Match: 84.42% Indels: 0 DB: 6	8 8 8	103* IIIIGGGAAIIIGGCCACAAACIAIGACAIIGGGGIIIGGGGGGGG
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32 LysaspGlyLysalaPheHisProThrTyrGluGluLysLeuLysPheValalaLeuHis	7 d	
Db 74 AAAGATGGCAAAGCATTTCAFCCAACTTAFGAAAAAATTGAAGCTTGFGGCACTGCAT 133	à	412 AspGluIleValProValTyrArgArgAspCysHisGluGluValTyrAlaGlySerHis 4

52 LysGlnValLeuLeuGlyProTyrAsnProAspThrSerProGluValGlyPhePheAsp 71		172 LeuargLeuGluGlnGlnLysGlnGlnIleWetAlaalaLeuasnSerGlnThralaval 191	### ### ##############################	
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		AUTHORS LIU., CANALII.L.K., Haddad, H.K. and Papadopoulos, V. Molecular cloning, genomic organization, chromosomal mapping and subcellular localization of mouse PAP?: a PBR and PKA-RIalpha associated protein Journal Gene 308, 1-10 (2003) REFERENCE 2 (bases 1 to 1572) AUTHORS Liu.J., Toblin,D., Tasken,K. and Papadopoulos,V. TITLE Direct Submission JOURNAL Submission JOURNAL Submitted (13-SEP-2002) Department of Cell Biology, Georgetown Univ./Medical Center, 3900 Reservoir Rd. NW, Washington, DC 20057, USA.	FEATURES Location/Qualifiers 13572 13572 Lording	ORIGIN Alignment Scores: 8.91e-140 Length: 3572 Score: 1983.00 Matches: 385 Percent Similarity: 94.00% Conservative: 22 Best Local Similarity: 88.91% Mismatches: 25 Query Match: 9.83% Indels: 2 DB: 9 Gaps: 0 US-09-762-594-7 (1-463) x AY150218 (1-3572) Oy 32 LysAopGlyLysAlaPheHisProThrTyrGluGluLysPheValAlaLeuHis 51 Oy 31 LysAopGlyLysAlaPheHisProThrTyrGluGluLysPheValAlaLeuHis 51 Db 315 AAAGATGGCAAAGCATTTCATCCAACTTATGAAGAAAATTGAAGCTTGTGGCACTGCAT 374

Alignment Scores: 7.18e-136 Length: 3492 Score: 1931.00 Matches: 368 Score: 90.55\$ Conservative: 25 Best Local Similarity: 84.79\$ Mismatches: 39 Query Match: 5 Gaps: 1	-09-762-594-7 (1-463) x AJ720620 (1-3492) 32 LygAspGlyLysAlaPheHisProThrTyrGluGluLysLeuLysPheValAlaLeuHis 51	Storm Additional Control of the Cont	Oy 72 ValleuGlyAsnAspArgArgArgGluTrpAlaAlaLeuGlyAsnMetSerLysGluAsp 91	Oy 92 AlaMetValGluPheValLysLeuLeuAsnLySCysCysCysProLeuLeuSerAlaTyrVal 111 DD 486 GCTATGACAGAATTTGTAAAGCTCCTAAATAGGTGCTGCCACTTGTTCTCAACGTATGTT 545	Oy 112 AlaSerHisBArgIleGluLysGluGluGluGluLysBArgArgLysBAlaGluGluBrg 131	Oy 132 ArgGlnArgGluGluGludRrgGluArgLeuGlnLysGluGluGluGluLysArgLysArg 151	Qy 152 GluGluGluAspArgLeuArgArgGluGluGluGluArgArgArgIleGluGluGluArg 171 	Oy 172 LeuArgLeuGluGlnGlnLysGlnGlnIleMetAlaAlaLeuAsnSerGlnThrAlaVal 191 	Qy 192 GlnPheGlnGlnTyralaalaGlnGlnTyrProGlyAsnTyrGluGlnGlnGlnGlnIleLeu 211 Db 786 CAGTTCCAGCAGTATGCTGCTCAGCAGTATCCCGGCAACTATGAACAGCAGCAGCAGATCCTC 845	Qy 212 IleargGlnLeuGlnGluGlnHisTyrGlnGlnTyrLysHisGlnAlaGluGlnThrGln 231 Db 846 ATTCGACAGCTCCAAGAGCAGCACTATCAACAGTACATGCAGCAGTTGTATCAAGTCCAG 905	Oy 232 ProhlaGinGinGinAlahlaLeuGinLysGinGinGluValValWetAlaGlyAlaSer 251 	252 LeuproAlaserseriyevalAsıThırAlaGlyAlaSerAspThrLeuSerVal 26	Oy 270 AsnGlyGlnAlaLysThrHisThrGluAsnSerGluLysValLeuGluProGluAlaAla 289	Oy 290 GluGluAlaLeuGluAsnGlyProLysAspSerLeuProValIleAlaAlaProSerMet 309	Qy 310 TrpThrArgProGlnIleLysAspPheLysGluLysIleArgGlnAspAlaAspSerVal 329 Db 1146 TGGGCACGACCCCAGATAAAAGACTTCAAAGAAAATCCGGCAGGATGCAGACTCTGTG 1205	Oy 330 IleThrValargArgGlyGluValValThrValArgValProThrHisGluGluGlySer 349
Qy 411 uAspGluIleValProValTyrArgArgArgAspCysHisGluGluValTyrAlaGlySerHi 431 Db 1454 GGATGAGGTCTGTGTACCGACGGACTGTCATGAGGAGGTGTATGCTGGCAGCCA 1513 Qy 431 sGlnTyrProGlyArgGlyValTyrLeuLeuLysPheAspAsnSerTyrSerLeuTrpAr 451 Db 1514 TCAATATCCAGGAGAGGAGTCTATCTCCTCAAGTTTGACAACTCTTTGTGGCG 1573	451 GSerLysSerValTyrTyrArgValTyrTyrThrArg 463 	AJ720620 3492 bp mRNA linear VRT 30-SEP-2004 ION Gallus gallus mRNA for hypothetical protein, clone 21m6. ON AJ720620		<pre>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.</pre>	erzek A.M., Arakawa, H., Bezzubov, Y., Zaim, J., r, S., Blagodatski, A., Kostovska, D., Koter, M., ci, P., Hayashizaki, Y. and Buerstedde, J. M. from bursal lymphocytes to facilitate gene	function analysis AL Unpublished CE 2 (bases 1 to 3492) RS Caldwell, R.B.	Direct Submission L Submitted (20-MAY-2004) Caldwell R.B., GSF - Forschungszentrum, Institut fuer Molekulare Strahlenbiologie, Ingolstaedter Landstr. 1, D-85764 Neuherberg, GERMANY				/locus_tag="RCJMB04_21m6" R <150 /locus_ag="RCJMB04_21m6" 51 1610	/locus_tag="RCJMB04_21m6" /note="ORF1" /codon_start=1 /product="hypothetical protein"		ALHKQVLLGEPYNEDTCPEVGFEDRLGNDRRKEWAALGNNSKOEAMTERVKLLINKCHL FSTYUTSHKI TERESERRKRREBESERRLOKREBEEBRLRREBEEBR RRI EBERLEMBEQKQQINMALLOKOOYAMOFOOYPEOYALGOYAGOYEGOYGOOTLI ROLOGOKHYOO YMQQLYQVQLAQQQAALQKQQEAVVAAAGTPLTTASKVNVPAQGDMFSINGQASAHTD	VYTUVRVPTHEEGALEINGFRUSVPYTAAPSMWARPQIKUFKEKIRQDAUSVITVGRGE VVTUVRVPTHEEGSYLFWEFATDSYDIGFGVYFEWTDSPNTAVSVHVSESSDDEBEEE NAASBEEKAKKNANKPQLDEIVLVYRRDCHEEVYAGSHQYPGRGVYLLKFDNSYSLWRS KTVYYRVYYTR	3'UTR 1611>3492 /locus_tag="RCJMB04_21m6"

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TyrLeuPheTrpGluPheAlaThrAspSerTyrAspIleGlyPheGlyValTyrPheGlu 36	370	390 GluGluGluGluGluAsnValThrCysGluGluLysAlaLysLysAsnAlaAsnLysPro 4 :::	410 LeuleuAspGlulleValPrOValTyrArgArgAspCysHisGluGluValTyrAlaGly 	erLeu 4		AY644721 1598 bp mRNA linear MAM 07-JUL	DEFINITION Sus scrota peripherial benzodiazepine receptor associated protein mRNA, complete cds. ACCESSION AY644721 VERSION AY644721 GT-49615356	Sus scrofa (pig) Sus scrofa (pig) Filestore (protection of the protection of the pro	EMERENCE 1 (bases 1 to 1598) AUTHORS Zhang, K., Petit-Paris, Luthell, D., Favreau, F., Tallineau, C.,	Inserm ERM 3 culte de Mede etrie, B.P. 5	ocation/Qualifiers	us scrota RNA" xon:9823"		/protein id="AAfr66937.1" /db_xref="G1:49615357" /translation="MYBEVKLINRCCHLFSTYVASHKIEKEEQEKKRKEEEERRRREE EERERLQKEEEKRRREEEERLRREEEERRRIEEEGRRIEEGOKQQIMAALNSQTAVLFQ	QYARQYEYEYEKEGOZULIKOLOEBOYYQQYRQDIYYQQYALQQQAALQXQOEAYAYGAGSEL PTSSKYNYTPAFGDWMSYNGQARAHSDNSEKELEPETABEALENGPKESLPVTAAPENW TRPQIRDFKEKIRQDSDSVITVGRGEVVTVRVPTHEEGSYLFWEFATDNYDIGFGVYF EWTDSPRYAVSVHYDSESSEHDDDESEEBINISEBERAKKAKAANKPVLDEIVPVYRRDCHEE VYAGCSHOY PGAGIVYI I KPINAS SCHADDESEERIKAKKAANKPVLDEIVPVYRRDCHEE	polyA_signal 15441549 ORIGIN	nt Scores: 7.73e-119 Length: 0.: 1699.50 Matches:	Percent Similarity: 93.30% Conservative: 21 Best Local Similarity: 87.67% Mismatches: 24 Query Match: 70.99% Indels: 1

us-09-762-594-7.rge

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

DEFINITION

RESULT 12 BC034563

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361 ATGCAGCAGTTGTATCAAGTCCAGCTTGCACACAGCAACAGGCAGCATTACAGAAACAACAG 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 ArgArgArgIleGluGluGluArgLeuArgLeuGluGlnGlnLysGlnGlnIleMetAla
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S Strausberg R.L. Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Colling, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mallek, J.A., Gunaratne, P.H., Richards, S.,

Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Youngh, A.C., Shevchenko, Y.,

Butterfield, Y.S., Krzywinski, M.I., Skalaka, U., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalaka, U., Sanilus, D.E.,

Butterfield, M. Schein, J. E., Jones, S.J., and Marra, M.A.
BC034563 3037 bp mRNA linear PRI 19-NOV-2003 Homo sapiens acyl-Coenzyme A binding domain containing 3, mRNA (cDNA clone IMAGE:3858463), partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAR Plate: 21 Row: c Column: 15.
Location/Qualifiers
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing Center
Center code: BMT-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunartene, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH MGC Project URL: http://mgc.nci.nih.gov
On Sep 16, 2003 this sequence version replaced gi:21961496.
Contact: MGC help desk
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                                                                                                                      1224 AGGTCTAAATCAGTCTACTACAGAGTCTATTACACTAGA 1262
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                                                                        451 ArgSerLysSerValTyrTyrArgValTyrTyrThrArg
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Tissue Procurement: DCTD/DTP
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Direct Submission
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REFERENCE AUTHORS TITLE JOURNAL

REMARK

COMMENT

JOURNAL MEDLINE PUBMED

TITLE

180 183 240 203 300

120

360

/organism="Homo sapiens" /mol_type="mRNA"

FEATURES

165 ArgArg11eGluGluArgLeuArgLeuGluGlnGlnLysGlnGlnI1eMetAlaAla	Db 62 AGACGGATAGAAGAAGAAGAGCTTCGGTTGGAGCAGCAAAAGCAGCAGATAATGGCAGCT 121 Qy	205 TyrGludInGluDILILeLeulleArgGluLeudInGludInGludInTyrLy8 [Oy 225 HisGlnalaGluGlnThrClnProAlaGlnGlnGlnAlaAlaLeuGlnLysGlnGlnGluGlu 244	ValValMetAlaGlyAlaSerLeuProAlaSerSerLyBValAenThrAlaGlyAlaSer ::: :::	Qy 265 AspThrLeuSerValAsnGlyGlnAlaLysThrHisThrGluAsnSerGluLysValLeu 284 ::: :::	Qy 285 GluProGluAlaAlaGluGluAlaLeuGluAsnGlyProLysAspSerLeuProValIle 304	Qy 305 AlaAlaProSerMetTrpThrArgProGlnIleLysAspPheLysGluLysIleArgGln 324	Qy 325 AspAlaAspSerVall1eThrValArgArgGlyGluValValThrValArgValProThr 344 Db 542 GATGCAGATTCCGTGATTACAGTGGCCCAAGAGAAGTGGTCACTGTTCGAGTACCCACC 601	345 HisgludluGlySerTyrLeuPheTrpGluPheAlaThrAspSerTyrAspIleGlyPhe	Qy 365 GlyValTyrPheGluTrpThrAspSerFroAshAlaAlaValSerValHisValSerGlu 384	Qy 385 SerSerAspGluGluGluGluGluGluBsnValThrCysGluGluLysAlaLysLys 404	Qy 405 AsnAlaAsnLysProLeuLeuAspGluIleValProValTyrArgArgAspCysHisGlu 424	Qy 425 GluValTyrAlaGlySerHisGlnTyrProGlyArgGlyValTyrLeuLeuLysPheAsp 444	Oy 445 ABBSerTyrSerLeuTrpArgSerValTyrTyrArgValTyrTyrThrArg 463	SULT 14 714948 CUS CQ714948 EXPERIENTION Sequence 882 from Patent W002068579. CESSION CQ714948 RSION CQ714948.1 GI:42275805	KEFWRKDS . SCHWCE Homo sapiens (human) ORGANISM Homo sapiens ORGANISM Homo sapiens Enkaryota; Merazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
284 LeuGluProGluAlaAlaGluGluAlaLeuGluAsnGlyProLysAspSerLeuProVal	DD S41 CIGGAACCAGAAGCIGCAGAAGAAGCCCIGGAGAAIGGACCAAAAGAAICTCTCCAGIA 600	GINASPALAASDSerValileThrValArgArgGlyGluValValThrValArgValPro	Qy 344 ThrHisGluGluGlySerTyrLeuPheTrpGluPheAlaThrAspSerTyrAspIleGly 363 Db 721 ACCCATGAAGAAGGATCATATTTTTTTTTTTTTTTTTTT	Oy 364 PheGlyValTyrPheGluTrpThrAspSerProAsnAlaAlaValSerValHisValSer 383 	Qy 384 GluserSerAspGluGluGluGluGluGluAsnValThrCysGluGluLysAlaLys 403 	Oy 404 LyskanalaaksnLysProLeuLeuAspGlulleValProValTyrargArgAspCysHis 423 	Oy 424 GluGluValTyrAlaGlySerHisGlnTyrProGlyArgGlyValTyrLeuLeuLysPhe 443 	Oy 444 ASPASNSETJYRSELEUTRPARGSELVABSERVAllYFTYRARGVAlTYTHRARG 463	RESULT 13 AX677275 LOCUS AX677275 BETINITON Sequence 53 from Patent W002086122.	ACCESSION AX677275.1 GI:29334680 KEYWORDS . SOURCE Homo sapiens (human)	Homo Eukar Mamma	AUTHORS Legrain, P. and Daviet, L. TITLE Protein-protein interactions in adipocytes JOURNAL Patent: WO 02086122-A 53 31-OCT-2002;	FEATURES 17.01-19.01/Qualifiers Source 1961 //organism="Homo sapiens".	/mol_type="unassigned DNA" /db_xref="taxon:9606" ORIGIN	Alignment Scores: Pred. No.: Pred. No.: Score: Score: Scoret Similarity: Best Local Similarity: Ouery Match: 62.87% Indels: O Best Gaps:	US-09-762-594-7 (1-463) x AX677275 (1-961) Qy

458 841 PAT 17-JUL-2003

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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. 1 (bases 1 to 2714)

S Valenzuela, D., Yuan, O., Hoffman, H., Hall, J. and Rapiejko, P. Secreted proteins and polynucleotides encoding them ALPHAGENE INC.

S Homo sapiens (human)

PN JP 2002536973-A/16

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PD 05-NOV-2002

PF 18-FEB-2000 JP 2000599860

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29-NOV-1999 US 60/157847, 29-NOV-1999 US 60/18711 PL DARIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PR 19-FEB-1999 US 60/120680,23-APR-1999 US 09/298733 PR 17-AUG-1999 US 60/149639,23-SEP-1999 US 60/155686 PR 01-OCT-1999 US 60/157247,29-NOV-1999 US 60/167823 PR 29-WV-1999 US 60/167822, PEBB-2000 US 60/167821 PI DARIO VALENZUELA,OLIVE YUAN, HEIDI HOFFMAN, JEFF HALL, PETER PI RAPIEJKO PC C12N15/09,A61R38/00,A61P3/10,A61P5/14,A61P11/00,A61P1/06, PC
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AG1P31/18,AG1P31/20,AG1P31/22,AG1P37/00,AG1P37/06,C07K14/435,
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PC A61P21/04,A61P25/14,A61P27/02,A61P29/00,A61P31/04,A61P231/10,
PC A61P31/12,
PC A61P31/18,A61P31/20,A61P31/22,A61P37/00,A61P37/06,C07K14/435,
PC C12NS/10,
PC C12NS/10,
PC C12P19/34//(C12P19/34,C12R1:91),C12N15/00,C12N5/00,A61K37/02
CC Secreted proteins and polynucleotides encoding them FH Key
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                                     TyrLeuLeuLysPheAspAsnSerTyrSerLeuTrpArgSerLysSerValTyrTyrArg
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/organism="Homo sapiens"
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Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses
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(c) 1993 - 2005 Compugen Ltd.
                                                                                                                   nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                The invention provides isolated peripheral-type benzodiazepine receptor (PBR) associated proteins (PAPs) and nucleic acids encoding the PAP polynucleotides are a source of primers and probes for detection, isolation and amplification. PAP ligands or substrates or antibodies can be labeled and used to detect PAPs, in the diagnosis and prognosis of disease associated with increased cell proliferation, such as cancer, or reduced cell death. The diagnostic methods of the invention can be predictive of diseases involving PBR including gallstones, proliferation, Schnyder's corneal crystalline dystrophy, brain disorders including Altheimer's disease, cholesterol metabolism, Tellurium proliferation, Gamyelinization, Charcot Marie tooth disease, Pelizaeus Muriabacher disease, Multiple solerosis, and SIA. The methods may also be effective in prophylactic treatments, or in screening for compounds effective in prophylactic treatments, or in screening for compounds effective in prophylactive treatments. The PAPs may be used to identify and the control of the compounds of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agents which modulate PBR activity. Inhibitors of PAP may be used in the treatment or amelioration of conditions such as stress and stroke, cancer, neurodegenerative disorders, developmental disorders, infertility and immune disorders. The present sequence represents a cDNA encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247
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                                                                                                      ds; gene; cytostatic; nootropic; neuroprotective; antiparkinsonian; anticonvulsant; antiviral; neuroleptic; central nervous system; POSH polypeptide; POSH-associated protein; POSH-AP; HERPUDI; Ubiquitin ligase; antiviral agent; anti-apoptotic agent; anti-cancer agent; secretory pathway traficking inhibitor; neurological disorder progression disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; schizophrenia;
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                                                                                    protein associated DNA #44.
                 ADS34290 standard; DNA; 3560 BP
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2003US-0460792P
2003US-04642BSP
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2003US-0479317P
2003US-0499317P
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2003US-0456640P.
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                                                                                                                                                                                   Niemann-Pick's disease
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04-APR-2003;
21-APR-2003;
09-MAY-2003;
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30-MAY-2003;
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19-JUN-2003;
19-JUN-2003;
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16-SEP-2003;
10-NOV-2003;
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20-MAR-2003;
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POSH-associated disease is viral infection, POSH-associated cancer or POSH-associated neurological disorder. The methods are useful for treating or preventing POSH-associated neurological disorder in a subject e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, schizophrenia, Niemann-Pick's disease. This sequence corresponds to a
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                                                          ValArgArgGlyGluValValThrValArgValProThrHisGluGluGlySerTyrLeu
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                   ArgProGlnIleLysAspPheLysGluLysIleArgGlnAspAlaAspSerValIleThr
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2003US-0464285P.
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The invention relates to an isolated, purified or recombinant complex (I) comprising a POSH polypeptide and a POSH-associated protein (POSH-AP) (a) or HERPUDI and a Ubiquith ligase (b). Methods using (l), (a) or (b) are useful for identifying a agent that modulates an activity of a POSH polypeptide or POSH-AP, for identifying an antiviral agent, an anti-cancer agent, an agent that inhibits trafficking of a protein through the secretory pathway, an agent that inhibits trafficking or progression of a neurological disorder, an agent that inhibits the progression of a neurological disorder, an agent that modulates a POSH cused for treating a viral infection, for inhibiting an activity of a POSH-associated disease is viral infection, POSH-associated cancer or POSH-associated disease is viral infection, POSH-associated cancer or treating or preventing POSH-associated methods are useful for treating POSH-associated meurological disorder. The methods are useful for treating POSH-associated meurological disorder in a subject treating or preventing POSH-associated meurological disorder in a subject endicophrenia. Niemann-Pick's disease, Huntington's disease, schizophrenia.
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17-JUN-2003; 2003US-0479317P.
19-JUN-2003; 2003US-0480215P.
19-JUN-2003; 2003US-0480376P.
08-AUG-2003; 2003US-0493860P.
28-AUG-2003; 2003US-0498634P.
16-SEP-2003; 2003US-0503931P.
10-NOV-2003; 2003WO-US035112.
05-FEB-2004; 2004WG-US003600.
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The invention relates to an isolated, purified or recombinant complex (I) comprising a PoSH polypeptide and a PoSH-associated protein (PoSH-AP) (a) or HBRFUDI and a Ubiquitin ligase (b). Methods using (I), (a) or (b) are useful for identifying an agent that modulates an activity of a poSH polypeptide or PoSH-AP, for identifying an antiviral agent, an anti-apoptotic agent, an anti-cancer agent, an agent that inhibits trafficking of a protein through the secretory pathway, an agent that inhibits the progression of a neurological disorder, an agent that inhibits the progression of a neurological disorder, an agent that modulates a PoSH function, an agent that modulates a HERPUDI function. The methods can be useful for treating a viral infection, for inhibiting an activity of a PoSH-associated disease is viral infection, PoSH-associated cancer or PoSH-associated disease is viral infection, PoSH-associated cancer or PoSH-associated neurological disorder. The methods are useful for treating or preventing PoSH-associated neurological disorder in a subject eg. Alzheimer's disease, Parkinson's disease, Huntington's disease, ceg. Alzheimer's disease, Parkinson's disease, Huntington's disease, corresponds to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated, purified or recombinant complex, useful for identifying an antiviral, anti-apoptotic or anti-cancer, comprising POSH polypeptide POSH-associated protein (POSH-AP).
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Ben-Avraham D,

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ADS34287 standard; DNA; 3598

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neuroprotective; antiparkinsonian;
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                                                         POSH protein associated DNA #41.
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04-APR-2003; 2003US-0460732P.
12-APR-2003; 2003US-0460732P.
09-MAY-2003; 2003US-0469462P.
15-MAY-2003; 2003US-047337B.
15-MAY-2003; 2003US-047327P.
30-MAY-2003; 2003US-047327P.
30-MAY-2003; 2003US-0475825P.
13-JUN-2003; 2003US-0479317P.
19-JUN-2003; 2003US-0480215P.
19-JUN-2003; 2003US-0480376P.
19-JUN-2003; 2003US-049866P.
28-AUG-2003; 2003US-0503931P.
16-SEP-2003; 2003US-0503931P.
16-NOV-2003; 2003US-0503931P.
16-NOV-2003; 2003US-0503931P.
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19-MAR-2003; 2003US-0455760P-
20-MAR-2003; 2003US-0456640P-
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                                                           PheTrpGluPheAlaThrAspSerTyrAspIleGlyPheGlyValTyrPheGl
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05-MAR-2003; 2003US-0452284P.
19-MAR-2003; 2003US-0455760P.
03-APR-2003; 2003US-0456640P.
03-APR-2003; 2003US-0460528P.
04-APR-2003; 2003US-0460722P.
21-APR-2003; 2003US-046428P.
09-MAY-2003; 2003US-046428P.
20-MAY-2003; 2003US-047378P.
20-MAY-2003; 2003US-047378P.
19-JUN-2003; 2003US-047317P.
19-JUN-2003; 2003US-0479317P.
19-JUN-2003; 2003US-0480215P.
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The invention relates to an isolated, purified or recombinant complex (I) comprising a POSH polypeptide and a POSH-associated protein (POSH-AP) (a) or (B) are useful for identifying an agent that modulates an activity of a poSH polypeptide or POSH-AP, for identifying an anti-viral agent, an anti-cancer agent, an activity of a notice apoptedic agent, an anti-cancer agent, an agent that inhibits trafficking of a protein through the secretory pathway, an agent that inhibits trafficking progression of a neurological disorder, an agent that inhibits the progression of a neurological disorder, an agent that modulates a POSH function, an agent that modulates a HERPUDI function. The methods can be used for treating a viral infection, for inhibiting an activity of a POSH-ABSOCiated disease is viral infection, POSH-aBSOCiated cancer or POSH-aBSOciated neurological disorder. The methods are useful for treating or preventing POSH-aBSOCiated neurological disorder. The methods are useful for treating or preventing POSH-aBSOCiated neurological disorder. The methods are useful for treating or preventing POSH-aBSOCiated neurological disorder in a subject e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, Barkinson's disease, Huntington's disease, Barkinson's disease, Huntington's disease,
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                                                                                                                                                                                                                                                                          antiviral, anti-apoptotic or anti-cancer, comprising POSH polypeptide POSH-associated protein (POSH-AP).
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16-SEP-2003; 2003US-0503931P.
10-NOV-2003; 2003WO-US035712.
05-FEB-2004; 2004WO-US003600.
02-MAR-2004; 2004US-054985EP.
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587 G; 464 T; 0 U; 0 Other; Sequence 2140 BP; 628 A; 461 C;

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The invention relates to polymucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to prytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
(AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding polypeptides with cytokine-like activities, useful
Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
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J, Zhang J, Ren F, Chen R, Wang
Goodrich R;
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nao QA, Wang D, Wang
Yang Y, Wejhrman T,
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2000US-00560H75.
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27-APR-2000;
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01-SEP-2000;
15-SEP-2000;
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30-NOV-2000;
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Ma Y, Zha
Xue AJ, )
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Matches:
Conservative:
Mismatches:
Indels: Gaps: US-09-762-594-7 (1-463) x AAK52051 (1-3399) 5.15e-180 2042.00 94.68% 90.05% 85.30% Similarity: Percent Similarity: Best Local Similari Alignment Scores: Pred. No.: Score: 32 301 22 361 72 Query Match: DB: 유 엄

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progression of a neurological disorder, an agent that modulates a POSH function, an agent that modulates a HERPUD1 function. The methods can be used for treating a viral infection, for inhibiting an activity of a POSH-associated disease in a subject. The POSH-associated disease is viral infection, POSH-associated cancer or POSH-associated neurological disorder. The methods are useful for treating or preventing POSH-associated neurological disorder in a subject e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, schizophrenia, Niemann-Pick's disease. This sequence corresponds to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysAspGlyLysAlaPheHisProThrTyrGluGluLysLeuLysPheValAlaLeuHis
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                                                                                                                                                                                                                                                                                                     ds; gene; cytostatic; nootropic; neuroprotective; antiparkinsonian; anticonvulaant; antiviral; neuroleptic; central nervous system; POSH polypeptide; POSH-Associated protein; POSH-AP; HERPUDI; Ubiquitin ligase; antiviral agent; anti-apoptotic agent; anti-cancer agent; secretory pathway traficking inhibitor; neurological disorder progression disorder; Alzheimer's disease; Niemann-Pick's disease; Huntington's disease; schizophrenia;
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Sequences AAZ87205-Z87210 represent cDNAs encoding six human neurotransmission-associated proteins (NTAPs, AAY77121-Y77126). The present sequence, clone 998868, encodes a benzodiazepine receptor-associated protein, and was produced by extension of cDNA fragments isolated from a human kidney tumour cDNA library. The NTAPs are used for treatment or prevention of neurological diseases (e.g., Alzheimer's, Parkinson's or Huntington's diseases, cerebral neoplasms, or multiple screen for specific binding agents (potential agonists and antagonists). They can also be used to raise specific antibodies and to screen for specific binding agents (potential agonists and antagonists). NTAPs, and as a source of therapeutic antagonists (antisense, triplexforming or ribozyme molecules). The nucleic acids may also be used as a source of probes and primers for diagnosis or monitoring of NTAP condition of not identifying related sequences, and for chromosome mapping and for identifying related sequences, and for gene therapy. NTAP canteagonists are used to treat and prevent a wide range of cancers and immune disorders (e.g. AlDS, asthma, Crohn's disease, osteoporosis, viral or other infections). NTAP antibodies are used to detect NTAPs, for diagnosis or monitoring, as therapeutic antagonists, in competitive drug screens, and for affinity purification of NTAPs from natural sources
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                                                                                    New human neurotransmission associated proteins, useful for treatment, prevention and diagnosis of neurological disease, e.g. Alzheimer's disease, and antagonists for treating cancer or immune disorders.
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Alzheimer's disease; Parkinson's disease; Huntingcon's disease;
cerebrai neoplasm; multiple sclerosis; drug screening; gene therapy;
antagonist; cancer; AIDS; asthma; Crohn's disease; osteoporosis; ss.
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM88302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or petide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunoomodulatory activity and activity, tissue growth factor activity, immunoomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leuksemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                acids encoding polypeptides with cytokine-like activities, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            339 AAAGATGGCAAAGCATTTCATCCAACTTATGAAGAAAAATTGAAGCTTGTGGCACTGCAT
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Chen R,
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J, Zhang J, Ren F,
Goodrich R;
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Matches:
Conservative:
Mismatches:
Indels:
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27-APR-2000; 2000US-00560875.
20-UN-2000; 2000US-0059075.
19-JJL-2000; 2000US-005325.
15-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-0063351.
20-CT-2000; 2000US-0063325.
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Ma Y, Zhao QA, Wang D, Wang
Xue AJ, Yang Y, Wejhrman T,
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                                                         212 IleArgGlnLeuGlnGluGlnHisTyrGlnGlnTyrLysHisGlnAlaGluGlnThrGln
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The invention relates to an isolated, purified or recombinant complex (1) comprising a POSH polypeptide and a POSH-associated protein (POSH-AP) (a) or HERPUDI and a Ubfaultin ligase (b). Methods using (1), (a) or (b) are useful for identifying an agent that modulates an activity of a POSH polypeptoide or POSH-AP, for identifying an antiviral agent, an agent that inhibits trafficking of a protein through the secretory pathway, an agent that inhibits the progression of a neurological disorder, an agent that inhibits the function, an agent that modulates a POSH function, for treating a viral infection, for inhibiting an activity of a POSH in a cell, for treating a POSH-associated disease in a subject. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated, purified or recombinant complex, useful for identifying an antiviral, anti-apoptotic or anti-cancer, comprising POSH polypeptide and POSH-associated protein (POSH-AP).
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                                                                                                                                                         gene; cytostatic; nootropic; neuroprotective; antiparkinsonian;
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                                                                                                                                                              anticonvulsant; antivital; meutopiocective; diffiparkinsoni anticonvulsant; antivital; neuroleptic; central nervous system; POSH polypeptide; POSH-associated protein; POSH-AP; HERPUDI; Ubiquitin ligase; antiviral agent; anti-apoptotic agent; anti-cancer agent; secretory pathway traficking inhibitor; neurological disorder progression disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; schizophrenia; Niemann-Pick's disease.
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                                                                                                                       protein associated DNA #43.
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05-MAR-2003; 2003US-045284P.
19-MAR-2003; 2003US-0455760P.
20-MAR-2003; 2003US-0456640P.
03-APR-2003; 2003US-0460728P.
21-APR-2003; 2003US-046072P.
21-APR-2003; 2003US-04642P.
09-MAY-2003; 2003US-04737BP.
20-MAY-2003; 2003US-047327P.
30-MAY-2003; 2003US-047327P.
19-JUN-2003; 2003US-04731P.
19-JUN-2003; 2003US-0479317P.
19-JUN-2003; 2003US-0480316P.
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28-AUG-2003; 2003US-0498634P.
16-SEP-2003; 2003US-0503931P.
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05-FEB-2004; 2004WO-US003600.
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1514 TCAATATCCAGGAGAGAGAGTCTATCTCCTCAAGTTTGACAACTCCTACTCTTTGTGGCG 1573
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                              rValArgArgGlyGluValValThrValArgValProThrHisGluGlyGlyGlySerTyrLe
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     AGACTCTCCAAACACTGCTGTCAGCGTGCATGTCAGTGAGTCCAGCGATGACGACGAGGA
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                                                         CGACCTCAGATCAAAGACTTTCAAAGAGAAGATTCAGCAGGATGCAGATTCCGTGATTAC
                                                                                                                                                                                           rAspSerProAsnAlaAlaValSerValHisValSerGluSerSerAspGluGluGluGl
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05-MAR-2003; 2003US-045284P.
19-MAR-2003; 2003US-045560P.
20-MAR-2003; 2003US-0460526P.
03-APR-2003; 2003US-0460792P.
21-APR-2003; 2003US-0460782P.
09-MAY-2003; 2003US-046128P.
20-MAY-2003; 2003US-0471378P.
20-MAY-2003; 2003US-0471378P.
20-MAY-2003; 2003US-0471376P.
30-MAY-2003; 2003US-0471376P.
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     cancer or
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POSH-associated disease is viral infection, POSH-associated cancer o POSH-associated neurological disorder. The methods are useful for treating or preventing POSH-associated neurological disorder in a su e.g. Alzheimer's disease, Parkinson's disease, Wuntington's disease, Schizophrenia, Niemann-Pick's disease. This sequence corresponds to nucleic acid of the invention.
                                                                                              G; 1013 T; 0 U; 1 Other;
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385
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Matches:
Conservative:
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Best Local Similarity:
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                                       AACTACGAACAGCAGCAATTCTCATCCGCCAGTTGCAGGAGCAACACTATCAGCAGTAC
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                                                                                                                                                                                                                                                                                                                                             Isolated, purified or recombinant complex, useful for identifying an antiviral, anti-apoptotic or anti-cancer, comprising POSH polypeptide POSH-associated protein (POSH-AP).
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17-JUN-2003; 2003US-0479317P.
19-JUN-2003; 2003US-0480215F.
19-JUN-2003; 2003US-0480376F.
08-AUG-2003; 2003US-0493866P.
28-AUG-2003; 2003US-0498634P.
16-SEP-2003; 2003US-0503931P.
10-NOV-2003; 2003US-US03931P.
10-NOV-2003; 2004US-US035712.
05-FEB-2004; 2004US-US03500.
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Best Local Similarity:
Query Match:
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GluProGluAlaAlaGluGluAlaLeuGluAsnGlyProLysAspSerLeuProValIle 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; cytokine; cell proliferation;
nutritional supplement; immune modulation; autoimmune disorder;
haematopoiesis regulation; tissue growth; haemostasis; inflammation; ss.
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                     GTAGTAGTGGCTGGGTCTTCCTTGCCTACATCATCAAAAGTGAATGCAACTGTACCAAGT
                                                                                 GAACCAGAAGCTGCAGAAGAAGAAGAAGAATGGAACCAAAAGAATCTCTTCCAGTAATA
    ValValMetAlaGlyAlaSerLeuProAlaSerSerLysValAsnThrAlaGlyAlaSer
                                                                 265 AspThrLeuSerValAsnGlyGlnAlaLysThrHisThrGluAsnSerGluLysValLeu
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137. .757
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                                                                                                                                                                                                                                                            The invention relates to a complex between two interacting proteins in adipocyte cells, given in the specification. The proteins are identified by selecting a bait protein from a known adipocyte marker and then performing a yeast 2-hybrid selection to isolate prey proteins encoded by members of an adipocyte cDNA library. The proteins are designated SID (RTM) (selected interacting domains) proteins. Also included are a polymeptide in the adipocyte cells, a combinant host cell expressing at least one of the interacting compound in adipocyte cells, a SID (RTM) polymeptide comprising any of the 738 amino acid sequences given in the specification (including its fragment or variant), a sequences given in the specification (including its fragment or variant), a vector comprising the SID (RTM) polymucleotide, a recombinant host cell comprising the vector, a protein chip comprising the polymeptides and a recomplex, polymeptides, polymucleotides and compounds are useful for preventing or treating metabolic disorders such as obesity or diabetes. The complex, polymelectides are useful as probes or primers. The complex is particularly useful for identifying selected interacting domains SID (RTM) and including the protein interaction, thus exhibiting the therapeutic effect. The present sequence encodes a SID (ATM) and a such as obesity or diabetes.
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                                                                                                                                                 New complex between two interacting proteins in adipocyte cells, useful for identifying selected interacting domains that modulate protein interactions, or for preventing or treating metabolic disorders such as obesity or diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 961 BP; 315 A; 202 C; 252 G; 192 T; 0 U; 0 Other;
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1505.00
94.98%
90.60%
                14-MAR-2001; 2001US-0275734P.
                                                                            Daviet L;
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                                             (HYBR-) HYBRIGENICS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
CAATATCCAGGGGAGGAGGAGTCTATCTCCTCAAGTTTGACAACTCCTACTTTGTGGCGG
                                                                                                                                                  542 GAAGAAGAACAACGGTTGTCAAAAGAAGCCAAAAAAGAATGCCAACAAGCCTTTGCTG
                                                                                                                                                                                                                                                                                         602 GATGAGATTGTGCCTGTGTACCGACGGGACTGTCATGAGGAGGTGTATGCTGGCAGCCAT
                                                                                                                          AspSerProAsnAlaAlaValSerValHisValSerGluSerSerAspGluGluGluGlu
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                                                        PheTrpGluPheAlaThrAspSerTyrAspIleGlyPheGlyValTyrPheGluTrpThr
                                                                                         TTTTGGGAATTTGCCACAGACAATTATGACATTGGGTTTTGGGGTGTATTTTGAATGGACA
                                                                                                                                                                                                 GluGluGluAsnValThrCysGluGluLysAlaLysLysAsnAlaAsnLysProLeuLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster genomic polynucleotide SEQ ID NO 25378.
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11-JUL-2000; 2000US-00614150.
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genes from Drosophila and
interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-656860/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                      New secreted proteins and polynucleotides encoding them, which are derived from Homosapiens, useful for therapy, diagnosis, and research, well as nutritional sources or supplements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCCGCCAGTTGCAGGAGCAACACTATCAGCAGTACATGCAGCTGTATCAAGTCCAG
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                                                                                                                                                                                                                                    Rapiejko P;
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                                                                                                                                                                                                                                    Hoffman H,
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                                  99US-0120680P.
99US-00298733.
99US-0145639P.
99US-0155686P.
99US-0167247P.
99US-0167822P.
99US-0167822P.
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                                                                                                                                                                                                                                    Valenzuela D,
   18-FEB-2000;
                                  19-FEB-1999;
23-APR-1999;
17-AUG-1999;
                                                                                                                                                              15-FEB-2000;
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Pred. No.:
                                                                                       23-SEP-1999;
01-OCT-1999;
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              GlyPheGlyValTyrPheGluTrpThrAspSerProAsnAlaAlaValSerValHieVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                               ProThrHisGluGluGlySerTyrLeuPheTrpGluPheAlaThrAspSerTyrAspIle
                                                             LysProLeuLeuAspGluIleValProValTyrArgArgAspCysHisGluGluValTyr
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324 Gln---AspAlaAspSerVallleThrValArgArgGlyGluValValThrValArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide;
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11-JUL-2000; 2000US-00614150.
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discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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enriched library, clone:5330404D19 product:GOLGI RESIDENT PROTEIN
GCE60 homolog [Homo sapiens], full insert sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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High-efficiency full-length cDNA cloning
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PUBMED
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    Command line parameters:
-MODBL=frame+ p2n. model -DEV=xlh
-DB=EST -OFWT=fastap -SUFFIX=rst -MINMATCH=0.1 -LGODCL=0 -LGODEXT=0
-UNITS=b1ts -START=1 -END=-1 -MATRIX=b10sum62 -TRANS=human40.cdi -LIST=45
-UNITS=b1ts -START=1 -END=-1 -MATRIX=b10sum62 -TRANS=human40.cdi -LIST=45
-UNITS=b1ts -START=1 -END=-1 - MATRIX=000000000
-USR=USOP76254 @CGN 1 1 3437 @runat 1908205 171348 18327 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG SCRRES=0 -WAIT -DSPEDCCK=100 -LONGLOG
-DBV TIMBCUT=120 -WARN TIMBCUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPORT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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BC04553 H
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AV403085 M
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GC240143 A
BU153320 A
BU153320 A
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                   nucleic search, using frame_plus_p2n model
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Result 8

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TVRRGEVVTVRVPTHEEGSYLFWEFATDSYDIGFGVY FEWTDSPNAAVSVHVSESSDE
EEEEEENVTCEEKAKKNANKPLLDEIVPVYRRDCHEEVYAGSHQYPGRGVYLLKFDNS
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                                                                                                                                                                                                                                                                                     rns ranviva consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Ale (bases 1 to 3433)

RS Adachi, J., Alzawa, K., Akimura, T., Hara, A., Hashizume, W.,
Fukuda, S., Furno, M., Haragaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayasu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Katch, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Katch, H., Kawai, J., Kojima, Y., Matsuyama, T., Miyazaki, R., Ohno, M., Ohaato, N.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohaato, N.,
Okazaki, Y., Salto, R., Saltoh, H., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission

AL Submitted (16-JUL-2011) Yoshinide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-resegge:riken:jp,
Chara, 1-45-503-9216)
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LRREBEERRRI BEBERKLALBGQKQQIMAALNGTYAVQFQQYAQQYPGYYEQQOLILIRQ
LQEQHYQQYMQQLYQVQLAQQQAALQKQOEVVMAGASLLPASSKVNTAGASDTLSVNGQ
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Clone lib="RIKEN full-length enriched mouse cDNA library"
dev_stage="adult"
51. .1638
    Kawai,J.,
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Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/.

URL:http://genom.gsc.riken.jp/.
                                                                                                                                                                         RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="unnamed protein product; GOLGI RESIDENT PROTEIN GCP60 homolog [Homo sapiens] (SPTR|Q9H3P7, evidence: FASTY, 88.8%ID, 100%length, match=1575)
putative"
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Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                           FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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|protein_id="BAC26928.1"
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COMMENT

FEATURES 1.3560 /organiam="Homo sapiens" /mol_type="mRNA" /db	IGIN	DB: US-09-762-594-7 (1-463) x BC045533 (1-3560) QY	Qy 52 LysGlnValleuLeuGlyProTyrAsnProAspThrSerProGluValGlyPhePheAsp 71 Bb 382 AAGCAAGTTCTTATGGGCCCATATAATCCAGACACTTGTCCTGAGGTTGGATTCTTTGAT 441 Qy 72 ValLeuGlyAsnAspArgArgArgArgGluTrpAlaAlaLeuGlyAsnMetSerLysGluAsp 91 Db 442 GTGTTGGGGAATGACAGAGAGAAATGGGCCTGGGAAACATGTCTAAAGAGAT 501	AlametValGluPheValLysLeuLeuAsnLysCysCysProLeuLeuSerAlaTytVall
	Qy 351 LeuPheTrpGluPheAlaThrAspSerTyrAspIleGlyPheGlyValTyrPheGluTrp 370 Db 1297 CTATTTTGGGAATTTGCCACAGACAGTTATGACATTTGGGTTTATTTTGAATGG 1356 Qy 371 ThrAspSerProAsnAlaAlaValSerValHisValSerGluSerSerAspGluGluGlu 390 Db 1357 ACAGACTCTCCAAATGCTGTCAGTGTCCAGTGACTCCAGTGACGAGGAGGAG 1416	391 GluGluGluGluAsnValThrCysGluGluLysAlaLysLysAsnAlaAsnLysProLeu 410 1417 GAGGAGGAAGAAATGTCACTTGTGAAGAAAAAGGAAAAAAGAACGCCAACAACAAGCTTGT 147 411 LeuAspGluleValProValTyrArgArgAspCysHisGluGluValTyrAlaGlySer 430	1477 431 1537 451	BESULT 2 BEGG 533 BC045533 BC045534 ACCESSION BC045533.1 GLOCUE GLOCUE HOW Sapiens HTC. BLOCUE HCC. BLOCUE HCC. BLOCUE BLOCUE BLOCUE AUTHORS BLOCUE AUTHORS BLOCUE AUTHORS BLOCUE AUTHORS BLOCUE AUTHORS BLOCUE AUTHORS STREAM AUTHORS AUTHORS AUTHORS STREAM AUTHORS AU

FEATURES 11995 forganism="Homo sapiens" forganism="Homo sapiens" forganism="Homo sapiens" folone="manA" folone="taxon:9606" fissue type="70ary, pooled from 3 adults" folone Tib="NIH MGC_125" flab host="DH10B" floote="Vector: pCMV-SPORT6"	Alignment Scores: Pred. No.: Pred. No.: Score: Score: Percent Similarity: 94.69\$ Conservative: 94.03\$ Mismatches: 1 Gaps: 08-09-762-594-7 (1-463) x BC039575 (1-1995) Qy 32 LysAspGlLybyAlaPheHisProThrTyrGluGluLysPheValAlaLeuHis 51	314 ÀAAGATGGGAAAGGATTGATCCAAGTTATGAAGAAAATTGAAGCTTGTGGCACTGCAT 3 52 LysGlnValLeuLeuGlyProTyrAsnProAspThrSerProGluValGlyPhePheAsp 7	112 AlaSerHisArgIleGluLysGluGluGlu-LysArgArgLysAlaGluGluGluAr 131	Qy 171 gleuArgLeuGluGlnGlnLysGlnGlnIleMetAlaAlaLeuAsnSerGlnThrAlava 191 Db 734 GCTTCGGTTGGAGCAAAAGCAGCAGATAATGGCAGCTTTAAACTCCCAGACTGCCGT 793 Qy 191 IGlnPheGlnGlnTyrAlaAlaGlnGlnTyrProGlyAsnTyrGluGlnGlnGlnGlnGlnTleLe 211 Db 794 GCAGTTCCAGCAGTATGCAGCAGAAGTATCCAGGGAACTACGAACAGCACAACAGTATTCCAGGAACAGCAGCAACAGTATTCCAGGAACAGTATTCT 853 Qy 211 ulleArgGlnLeuGlnGluGlnHisTyrGlnGlnTyrLy8HisGlnAlaGluGlnThrGl 231 Db 854 CATCCGCAGTTGCAGGAGCAACACTATCAGCAGTACATGCACCAGTTGTATCAAGTCCA 913	231 nProladinalanladinalandinasis properties of the proladinalandinasis proladinalandinalandinasis proladinalandinasis proladinasis process. Transportation proladinasis proladinas prol
292 AlaLeuGluAsnGlyProLysAspSerLeuProValIleAlaAlaProSerMetTrpThr	Db 1222 GTGGGCCGAGGAGAGTGGTTCGAGTACCATGAAGAAGGATCATATCTC 1281 352 PheTrpGluPheAlaThrAspSerTyrAspIleGlyPheGlyValTyrPheGluTrpThr 371	412 AspGlulleValProValTyrArgArgAspCySHisGluGluValTyrAlaGlySerHis	RESULT 3 BC039575 LOCUS DEFINITION Homo sapiens, clone IMAGE:5725757, mRNA. ACCESSION BC039575 NERSION BC039575. I GI:25058702 KEYWORDS HTC. ORGANISM Homo sapiens (human) ORGANISM Homo sapiens CARATORN Homo sapiens ORGANISM Homo sapiens ORGANISM Homo sapiens Eukaryota: Mammalia; Eutheria; Primates; Cararrhini; Hominidae; Homo.		DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org contact: amadan@systemsbiology.org contact: amadan@systemsbiology.org contact: amadan@systemsbiology.org Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 84 Row: i Column: 21 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 15826851 This clone has the following problem: retained intron.

gene <1>1301 /gene="GOCAP1" /locus_tag="HCM1439"	Alignment Scores: 1.37e-183 Length: 1301 Score: 1883.00 Matches: 372 Percent Similarity: 86.11\$ Conservative: 0 Best Local Similarity: 86.11\$ Mismatches: 60 Query Match: 78.65\$ Indels: 0 DB: 9	US-09-762-594-7 (1-463) x AY403085 (1-1301) Oy 32 LygaAspGlyLygaAlaPheHisProThrTyrGluGluLysLeuLysPheyalAlaLeuHis 51		63 AAGCAAGTTCTTTGGGCCCATATAACCCAGACACGTCCCCTGAGGTTGGATTCTTTGAT	Cy /2 ValleuGiyAsnAspargArgGluTrpAlaAlaLeuGiyAsnMerSerlysGluAsp 91		243 GCGTCCCACAGAATAGAGAAGAAGAAGAAGAAGAAAAAAAA	Db 303 ИНИНИИНИИНИИНИИНИИНИИНИИНИИНИИНИИНИИНИИ	152 GluGluGluAspArgLeuArgArgGluGluGluGluArgArgArgIleGluGluGluArg	DD 363 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	192 GlnPheGlnGlnTyrAlaAlaGlnGlnTyrProGlyAsnTyrGluGlnGlnGlnGlnIleLeu 	Oy 212 IleargGlnLeuGlnGluGlnHisTyrGlnGlnTyrLysHisGlnAlaGluGlnThrGln 231	Qy 232 ProAlaGlnGlnGlnAlaAlaLeuGlnLy8GlnGlnGluValWalWetAlaGlyAlaSer 251	Qy 252 LeuprohlaSerSerLyeValAsnThrAlaGlyAlaSerAspThrLeuSerValAsnGly 271	Qy 272 GlnalaLysThrHisThrGluAenSerGluLysValLeuGluProGluAlaalaGluGlu 291	Cy 292 AlaLeuGluAshGlyProLysAspSerLeuProVallleAlaAlaProSerMetTrpThr 311	Oy 312 ArgProGlnIleLysAspPheLysGluLysIleArgGlnAspAlaAspSerVallleThr 331
Qy 291 uAlabeuGluAsnGlyProLysAspSerLeuProValIleAlaAlaProSerMetTrpTh 311 Db 1094 AGCCTGGAGAATGAACAAAGAATCTCTTCCAGTAATAGCAGCTCCATCCA	Qy 311 rArgProGInIleLy8AspPheLy8GluLy8IleArgGlnAspAlaAspSerValIleTh 331 Db 1154 ACGACCTCAGATCAAAGAGAAGATTCAGCAGATGCAGATTAC 1213 Qy 331 rValArgArgGlyGluValValThrValArgValProThrHisGluGluGlySerTyrLe 351 III	Oy 351 uPheTrpGluPheAlaThrAspSerTyrAspIleGlyPheGlyValTyrPheGluTrpTh 371	Qy 371 rAspSerProAsnAlaAlaValSerValHisValSerGluSerSerAspGluGluGluGluGluGluGluGluGluGluGluGluGluG	uGluGluGluAsnValThrCysGluGluLysAlaLysLysAsnAlaAsnLysProLeuLe 41	411 uhapglulleValProValTyrArgArgAspCysHisGluGluValTyrAlaGlySerHi 	Oy 431 sGlnTyrProGlyArgGlyValTyrLeuLeuLysPheAspAsnSerTyrSerLeuTrpAr 451	Oy 451 gSgrLygSerValTyrArgValTyrTyrThrArg 463 	RESULT 4	AY403085 LOCUS AY403085 DEFINITION Mus musculus GOCAPI gene, VIRTUAL TRANSCRIPT, partial sequence,		ORGANISM Mus musculus Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Bukaryota, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. REFERENCE 1 (bases 1 to 1301)	<pre>Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.</pre>		<pre>REFERENCE 2 (bases 1 to 1301) AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,</pre>	Adams,M.D. and Cargill,M. Direct Submission AL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude D Rockville, MD 20850, USA	CONTENT INTER BEQUETION WAS MADE BY BEQUENCING GENOMIC EXONS AND OIGEING FEATURES Location/Qualifiers Source 11301	/organism="mus musculus" /mol_type="qenomic DNA" /db_xref="taxon:10090"

Score: 1744.00 Matches: 340 Percent Similarity: 82.64\$ Conservative: 17 Best Local Similarity: 78.70\$ Mismatches: 75 Query Match: 9 Gaps: 0	33) x AY403083 (1-1301) 31yLysAlaPheHisProThrTyrGluGluLysEl	Db 3 AAAGATGCCAAAGCATTTCATCTATGAAGAAAAAATTGAAGCTTGTGGCAT 62 Qy 52 LygGlnValLeuLeulJyProTyrAsnProApThrSerProGluValGlyPheAsp 71	9	Db 123 GTGTTGGGGAATGAGAGGAGGAGGAGGCAGCCCTGGGAAACATGTCTAAAGAGGAT 182 Qy 92 AlaMetValGluPheValLysLeuLeuAsnLysCysCysCysProLeuLeuSerAlaTyrVal 111 QY 1	Db 183 GCCATGGTGGAGTTTGTCAAGCTCTTAAAAAGGTGTTGCCATCTTTTCAACATATGTT 242 Qy 112 AlaSerHisArg1leGluLysGluGluGluGluGluLysArgArgArgLysAlaGluGluGluArg 131	Db 243 GGTCCCACAAATAGAAAGAAGAAGAAGAAAAAAAAAAAA	3 03 NEKKHANININININININININININININININININININI	Qy 152 GluGluGluAspArgLeuArgArgGluGluGluGluArgArgArgIleGluGluArg 171 Db 363 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	Qy 172 LeuArgLeuGluGlnGlnLysGlnGlnIleMetAlaAlaLeuAsnSerGlnThrAlaVal 191	Qy 192 GlnPheGlnGlnTyralaAlaGlnGlnTyrProGlyAsnTyrGluGlnGlnGlnGlnIleLeu 211 Db 483 CAGTTCCAGCAGTATGCAGCCCAACAGTATCCAGGAACTACGAACAGCAGCAAATTCTC 542	Qy 212 IleArgGlnLeuGlnGluGlnHisTyrGlnGlnThrGln 231	Qy 232 ProAlaGlnGlnAlaAlaLeuGlnLysGlnGlnGluValValWathalaGlyAlaSer 251	252	Qy 272 GlnalaLysThrHisThrGluAsnSerGluLysValLeuGluProGluAlaAlaGluGlu 291		312 ArgProGlnIleLysAspPheLysGluLysIleArgGlnAspAlaAspSerValIleThr 33	332 ValhrgArgGluValuValThrValArgValProThrHisGluGluGluGlySerTyrLeu 35	Db 903 GTGGGCCGAGGAGAAGTGGTCACTGTTCGAGTACCCACCC
Db 843 AGACCACAAATCAAAGACTTTAAAGAGAAGATTCGGCAGGATGCAGATTCTGTGATTACA 902 Qy 332 ValArgArgGlyGluValValThrValArgValProThrHisGluGluGlyGsrTyrLeu 351 Db 903 GTACGTCGAGGAAAGTCGTCACCGTCCCGATCATCAGGAAGAATCATACTA	352 PheTrpGluPheAlaThrAspSerTyrAspIleGlyPheGlyValTyrPheGluTrpThr 	Qy 372 AspSerProAsnAlaAlaValSerValHisValSerGluSerSerAspGluGluGluGluUGlu 391 	Oy 392 GluGludsnValThrCysGluGluLysAlaLysLysAsnAlaAsnLysProLeuLeu 411 	Oy 412 AspGluIleValProValTyrArgArgAspCysHisGluGluValTyrAlaGlySerHis 431 	Qy 432 GlnTyrProGlyArgGlyValTyrLeuLeuLysPheAspAsnSerTyrSerLeuTrpArg 451 	Qy 452 SerLysSerValTyrTyrArgValTyrTyrThrArg 463 	H 5 083	z		ORGANISM Homo Sapiens Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 1301)	<pre>Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kepari Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy, Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J Adams,M.D. and Cargill,M.</pre>			Adams, M.D. and Cargill, M. TITLE Direct Submission JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA	COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. FEATURES Location/Qualifiers source 11301		/gene="GOCAP1" /locus_tag="HCM1439"	Alignment Scores: Pred. No.: 3.16e-169 Length: 1301

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CF240143 918 bp mRNA linear EST 05-AUG-2003
AGENCOURT 15112395 NICHD_XGC_Emb6 Xenopus tropicalis cDNA clone
IMAGE:6991831 5', mRNA sequence.
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                                                                                                                                                                                              CGGTTGGAGCAGCAAAAAGCAGCAGATAATGGCAGCTTTAAACTCCCAGACTGCCGTGCAG
                                                                  PheGlnGlnTyrAlaAlaGlnGlnTyrProGlyAsnTyrGluGlnGlnGlnIleLeuIle
                                                                                                                                333 ArgArgGlyGluValValThrValArgValProThrHisGluGluGlySerTyrLeuPhe
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                                                                                                                                                                182 CGCCAGTTGCAGGAGCAACACTATCAGCAGTACATGCAGCAGTTGTATCAAGTCCAGCTT
                                                                                                                                                                                                                                                               ProAlaSerSerLysValAsnThrAlaGlyAlaSerAspThrLeuSerValAsnGlyGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       542 GGCCGAGGAGAAGTGGTCACTGTTCGAGTACCCACCCATGAAGAAGGATCATATCTCTTT
                                                                                                  122 TTCCAGCAGTATGCAGCCCAACAGTATCCAGGGAACTACGAACAGCAGCAAATTCTCATC
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1 (hases 1 to 918)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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Xenopus tropicalis
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Site_2: SalI; cloned unidirectionally; oligo-df primed.
Site_2: salI; clones and constructed for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                   1142
                                                                                   1203 CAATATCCAGGGGAGAGAGTCTATCTCCTCAAGTTTGACAACTCCTACTTTGTGGAGG 1262
                                                                                                                                                                                                                                                                                             bp mRNA linear EST 03-SEP-2002
Homo sapiens cDNA clone IMAGE:6012409
                                                                    431
                                                                                                                                GlnTyrProGlyArgGlyValTyrLeuLusPheAspAsnSerTyrSerLeuTrpArg 451
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I (bases 1 to 884)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

Conteat: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Libr at:
http://inge.libr.gov
Plate: LibAM13203 row: k column: 02
High quality sequence stop: 645.
                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
GluGluGluAsnValThrCysGluGluLysAlaLysLysAsnAlaAsnLysProLeuLeu
                     AspGlulleValProValTyzArgAspCy8HisGluGluValTyzAlaGlySerHis
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Conservative:
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AGENCOURT 7938530 NIH_MGC_92
5', mRNA sequence.
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1295.00
91.53%
86.10%
54.09%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus
Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
I (basea I to 887)
Boardman, P.E., Sana-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA linear EST 25-NOV-2002
s cDNA clone ChEST142g8 5', mRNA
                                                                                                                                                                     GlyPheGlyValTyrPheGluTrpThrAspSerProAsnAlaAlaValSerValHisVal 382
                                                                                                                                                                                                                                                                                                                                                         LysAlaLysLysAsnAlaAsnLysProLeuLeuAspGluIleValProValTyrArgArg 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AspCysHisGluGluValTyrAlaGlySerHisGlnTyrProGlyArgGlyVal-TyrLe 440
                                                                               ProThrHisGluGluGlySerTyrLeuPheTrpGluPheAlaThrAspSerTyrAspIle 362
                                                                                                                                                                                                                                                                SerGluSerSerAspGluGluGluGluGluGlu-----GluAsnValThrCysGluGlu 400
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Department of Blomolecular Sciences
University of Manchester Institute of
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Pax: 01612360409
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603144828F1 CSEQCHL17 Gallus gallus
sequence.
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BU121963.1 GI:25332057
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Cloned unidirectionally. Primer: Oligo dT. Average insert
size 2.1 kb. Constructed by Invitrogen. Note: This is a
Xenopus Gene Collection (XGC) library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283 ValLeuGluProGluAlaAlaGluGluAlaLeuGluAsnGlyProLysAspSerLeuPro 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 RmloAd7 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Robert M. Grainger
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM14669 row: 1 column: 06
High quality sequence stop: 706.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 GlnGlnIleLeuIleArgGlnLeuGlnGluGlnHisTyrGlnGlnTyrLysHisGlnAla
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Conservative:
Mismatches:
Indels:
Gaps:
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|mol_type="mRNA"
|db_xref="texon:8364"
|clone="IMAGE:6991831"
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Numaciania, Butheria; Rodentia; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Muscatula (Nases it of 726)

1 (Joases it of 726)

2 (Acazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yangi, K., Tomaru, Y., Hasegawa, Y., Mogami, A., Kiyosawa, H., Badacelli, R., Hill, D.P., Bult, C., Golobori, T., Baldarelli, R., Hill, D.P., Bult, C., Golobori, T., Baldarelli, R., Hill, D.P., Bult, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Gissi, C., Godażk, A., Gough, J., Girmond, S., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gustincich, S., Hirokawa, N., Jackson, J.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Malleis, L., Marchionni, L., McKenaie, L., Miki, H., Nagashima, T., Narationni, L., Weckenie, L., Miki, H., Nagashima, T., Narationni, L., Weckenie, L., Miki, H., Nagashima, T., Raenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Schneider, C., Reed, J.C., Reed, J.C., Reed, J.C., Reed, J.C., Reed, J.C., Reed, J., Setou, M., Shimada, K., Schneider, C., Wanner, R. Mang, Y., Warane, M., Yang, I., Wanner, J., Manner, J., Warane, J., Manner, J., M
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Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (36C), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-reseggsc.riken.jp, URL:http://genome.gsc.riken.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Rukuda,S., Hashizune,W., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Takeda,Y., Waki,K., Watahiki,A., Muramateu,M. and Hayashizaki,Y.
Direct Submission
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
                                                                                                                          BY757076 RIKEN full-length enriched, blastocyst Mus
                                                                                                                                                                          clone IIC0048M22 3', mRNA sequence
Mus musculus (house mouse)
Mus musculus
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NotI and EcoRI. Ligate in double stranded adaptor containing Bsgi and BamHI sites [5' specycycogocoggaccogatcogaaaaaag] [5' aattetttttteggatecgggctgcacge] "
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CK600219 822 bp mRNA linear EST 22-JAN-2004
AGENCOURT_17895630 NIH MGC_234 Rattus norvegicus cDNA clone
IMAGE:7189739 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                          Conteact: Daniela S. Gerhard, Ph.D.
Conteact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rml0A07 Betheada, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Proturement: Howard Jacobs
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bisocience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM15046 row: b column: 09
High quality sequence stop: 695.
                                          GCTGTCAGTGTGCATGTCAGTGAGTCCAGTGACGAGGAGGAGGAGGAAGAAAATGTC
                         AlavalServalHisValSerGluSerSerAspGluGluGluGluGluGluGluBnVal
                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 822)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Rattus norvegicus
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96.44$
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Query Match:
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SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuArgArgGluGluGluGluArgArgArgIleGluGluGluArgLeuArgLeuGluGln 176
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                                                                                               prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                          /dev_stage="blastocyst"
/clone_lib="RIKEN full-length enriched, blastocyst"
                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                               1. .726
/organiem="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="I1C0048M22"
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
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                                                                                                                                                Location/Qualifiers
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95.45%
94.63%
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Best Local Similarity:
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/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_txef="taxon:8354"
/db_tissue_type="tailbud"
/dev_stage="embryo, stages 20-27"
/lab_hois="HH10B KGC Emb7"
/lone_lib="NICHD KGC Emb7"
/note="Vector: pCWV-SPORT6.1; Site 1: Not1; Site 2: EcoRV;
Cloned unidirectionally. Primer: oligo dT. Average insert size 2.1 kb. Constructed by Invitrogen. Note: This is a
Xenopus Gene Collection (XGC) library."
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DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM14632 row: 1 column: 15
High quality sequence stop: 715.
Location/Qualifiers
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233
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Xenopus tropicals

Xenopus tropicals

Relaziona; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

Xenopodinae; Xenopus; Silurana.

I (bases I to 993)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm.0A07 Betheada, MD 20892

Email: cgapbs-remail.nih.gov

Tissue Procurement: Robert M. Grainger

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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993 bp mRNA linear EST 04-AUG-2003
AGENCOURT 15064731 NICHD XGC_Emb7 Xenopus tropicalis cDNA clone
IMAGE: 6977632 5', mRNA sequence.
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GlnLysGlnGlnGluValValWatAlaGlyAlaSerLeuProAlaSerSerLysValAsn
                 CAGAAGCAGCAAGAAGTAGTGGTGGCTGGGGTTCATTGCCTGCGTCAGCAAGGTGAAC
                                                                 ThralaGlyAlaSerAspThrLeuSerValAsnGlyGlnAlaLysThrHisThrGluAsn
                                                                                                                                                                                                 SerLeuProVallleAlaAlaProSerMetTrpThrArgProGlnIleLysAspPheLys
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from proximal jejunums of 18 and 21 wk old steers, and distal ileums of 14 day old calves. proximal jejunum exposed to C. oncophora for 3 and 6 weeks, and distal ileum exposed to C. parvum for 7 dava"
                                                                                                                                                                                                                                                                                                                                                                                            GATGAACGGGAACGTCTGCAAAAGGAGGAAGAGAAAACGTAGGAGAGAAGAAGAAGG
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17000424186898 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
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Matches:
Conservative:
Mismatches:
Indels:
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Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Badig. 200 RmAD BARC-East, Beltsville, MD 20705, USA
Tel: 3015049416
Fax: 3015049416
Fax: 3015049416
Fax: 3015049416
Fax: 3015049416
Fax: 301504916
Fax: 3015049
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4101641 BARC 10BOV Bos taurus cDNA clone 10BOV8_D16 5', mRNA
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Sonstegard, T.S., Van Tassell, C.P., Matukumalli, L.K., Harhay,
G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
Production of EST from cDNA libraries derived from immunologically
activated bovine gut
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Pooled"
/dev_stage="Multiple"
/lab_host="DH10B T1 phage resistant"
/clone_lib="BARC 10BOW"
/note="Gorgan: Small Intestine; Vector: pAgen-1; Site_1:
BCORV; Site_2: Not1; Equimolar amounts of mRNA extracted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                       TyrLeuPheTrpGluPheAlaThrAspSerTyrAspIleGlyPheGlyValTyrPheGlu
                                                                                                                                                                                                                                                  TrpThrAspSerProAsnAlaAlaValSerValHisValSerGluSerSerAspGluGlu
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| GAGGAAGATGAGGGTAACGAACCCCAACAGCGAAGAGGCGAA-AAGAAGCCCAAC
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Location/Qualifiers
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/mol_type="mRNA"
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/sex="Male"
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/issue_type="cerebrum"
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/day_bet="withing"
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/done_lib="CSEQCHN72"
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KCORI; Site_2: Notl; This normalized library was
CONSTRUCTED from 1 million independent clones. CDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
ECORI, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bp mRNA linear EST 28-NOV-2002
gallus cDNA clone ChEST75205 5', mRNA
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1 (bases 1 to 773)

Boardman, P. E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                          567 TCATCCGCCAGTTGCAGGAGCAACACTATCAGCAGTACATGCAGCAGTTGTATCAAGTCC 626
                                                                                                                                                                                                                                                                                                                    erLeuProAlaSerSerLysValAsnThrAlaGlyAlaSerAspThrLeuSerValAsnG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                        687 cerreceracarcarcaaaagreaarecaacreraceaagraarargargreagraarg 746
                           447 GGCTTCGGTTGGAGCAGCAAGAAAGCAGCAGATAATGGCAGCTTTAAACTCCCCAGACTGCCG
                                                                                                                                                                                             eulleArgGlnLeuGlnGluGlnHisTyrGlnGlnTyrLysHisGlnAlaGluGlnThrG
                                                                                                                                                                                                                                                                                             lnProAlaGlnGlnAlaAlaLeuGlnLysGlnGlnGluValValMetAlaGlyAlaS
  rgLeuArgLeuGluGlnGlnLysGlnGlnIleMetAlaAlaLeuAsnSerGlnThrAlaV
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University of Manchester Institute of Science and Technology
(UMIST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. 773
/organism="Gallus gallus",
/nol_type="mRNA",
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="ChEST75205"
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Tel: 01612008930
Fax: 0161206409
Email: Simon.Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BU361227 773
603790024F1 CSEQCHN72 Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BU361227.1 GI:25869228
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Gallus gallus
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pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
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Patent No. 6703491
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PATENTI VET: 2.0
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66.43%
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   Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-270-767-26802/c
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LENGTH: 432
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Pred. No.:
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-MODEL=frame.
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-MINNATCH=0.1 -LOOPCL=0
-LOOPCXT=0
-LOOPCXT=0
-UNITS=bits -STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -TRR SCORE=pct -TRR MAX=100 -TRR MIN=0 -ALIGN=15
-MODEL=LOCAL. -OUTFMT=ptc -NORM=ext -HRABSIZE=500 -MINIEN=0 -NORU=6
-NORE-LOCAL. -OUTFMT=ptc -NORM=ext -HRABSIZE=500 -MINIEN=0 -NORU=6 -ICPU=3
-NORM=LOCAL. -OUTFMT=ptc -NORM=ext -HRABSIZE=500 -MINIEN=0 -NORU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NGG_CORRS=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TINREOUT=120 -WARN TIMBOUT=30 -TRIREADS=1 -XGAPOP=10 -LONGLOG
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 26802, A
Sequence 11257, A
Sequence 9, Appli
Sequence 9, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Appli
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 23, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 4611, Appl
                                                                                                           August 22, 2005, 18:56:48; Search time 244 Seconds (without alignments) 3104.902 Million cell updates/sec
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                                                                                                                                                                                                             RPRRPKVELFTVVTRVKVVL......DNSYSLWRSKSVYYRVYTR 463
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                           - nucleic search, using frame_plus_p2n model
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US-09-270-767-11257
US-09-291-4170-9
US-09-651-011A-3
US-09-651-011A-3
US-09-216-393B-80
US-09-688-188B-11
US-09-291-4170-11
US-09-248-796A-7812
US-09-520-781-23
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US-09-520-781-23
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Listing first 45 summaries
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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seq length: 200000000
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Perfect score:

Sequence:

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Scoring table:

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CAAGCATATCTCCTGTCTCTACAGCATGACCATAGGAGGCCGCACCCGCAGCACTCGCAG 1617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlnThrGlnProAlaGlnGlnGln-AlaAlaLeuGlnLysGlnGlnGluValValMetAl 248
Glu-------GluGluGluGluArgGluArgLeuGlnLysGluGluGluLysArgLys
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76
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                                                                  Sequence 9, Application US/096881888
; Patent No. 6656716
; GENERAL INPORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: MARTINEZ, RICARDO
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/09/688,188B
; CURRENT FILING DATE: 1999-04-14
; PRIOR FILING DATE: 1999-04-14
; PRIOR FILING DATE: 1999-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PATENTIN VUMBER: 60/081,784
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
DB:
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ORGANISM: Homo
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Pred. No.:
                                                                                                                                                                                                                                                                                                                    LENGTH: 3798
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|CACCGAGGACCTGGAGTCGGGCTCGCTGTCGCAGGAGCGCGGCGCAGTTAACAACCCGAC 328
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                                                                                    190 TGCTGCCCCAAGGCACCCATTTCCATTATCGTACCGATCTATCGCGGGGGGGTGCTACAA 131
                                                                                                                                                                                       130 CGAGGTCTACGTGGGCTCCCACTCCTATCCGGGCGAGGGCGTCTATTTGCTGAAGTTCGA 71
                                                                                                                                                                                                                                                                                   RESULT 2
US-09-270-767-11257/c
US-09-270-767-11257/c
Sequence 11257, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ 1D NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ 1D NO 11257
LENGTH: 569
                                                                                                                                                                                                                              pAsnSerTyrSerLeuTrpArgSerLysSerValTyrTyrArgValTyrTyrThrArg 463
                   ValArgValProThrHisGluGlu-GlySerTyrLeuPheTrpGluPheAlaThrAspSe
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                                                         ----GluGluGluGluAsnValThrCysGluGluLysAlaLysLysAsn
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Matches:
Conservative:
Mismatches:
Indels:
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  rValHisValSerGluSerSerAspGluGlu
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; ORGANISM: Drosophila melanogaster
US-09-270-767-112$7
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                                                                                                                                                                                                                                                                                                   298 sAspSerLeu---ProVallleAlaAlaProSerMetTrpThrArgProGlnIleLysAs 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 ArgGluGluGluAspArgLeuArgArgGluGluGluGluArgArgArglleGluGluGlu 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 Glu------GluGluGluArgGluArgLeuGlnLysGluGluGluLysArgLys 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09651011A
Sequence 3, Application US/09651011A
Patent No. 6346416
GENERAL INFORMATION:
APPLICANT: Lex M. Coweert
TITLE OF INVENTION: ANTISENSE MODULATION OF HPK/GCK-LIKE KINASE EXPRESSION
FILLE REPRENCE: FTS-0168
CURRENT APPLICATION NUMBER: US/09/651,011A
NUMBER OF SEQ ID NOS: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 ArgileGluLysGluGluGluGluLysArgArgLysAlaGluGluGluArgArgGlnArg 134
                                                                                                                                                                                                                                                                                                                      GinThrGlnProAlaGinGlnGln-AlaAlaLeuGlnLysGlnGlnGluValValMetAl
                                                                                                                                                                                                                                                                   1770 AGGCAGAGTATIGGAGCCACCAGTGCTTCCCGATCAGAGTCTTTTCCAATGGCAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317 pPheLysGluLysIleArgGlnAspAlaAspSerVallleThrValArgArg 334
                                                                                                                                                                            268 rValAsnGlyGln---AlaLysThrHisThrGluAsnSerGlu----
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Mismatches:
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Matches:
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226.50
49.58%
30.08%
9.46%
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ORGANISM: Homo sapiens
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Query Match:
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US-09-651-011A-3
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1710 GGTGGAAGATAGATTTAGGAAACTAACCAGGTCCCCTGAAGCCCAGTCTAAGCAGAC 1769
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                                                              ----LysValLeuGluPro-----GluAlaAlaGluGluAlaLeuGluAsnGlyProLy 298
      281
                                                                                                                          sAspSerLeu---ProValIleAlaAlaProSerMetTrpThrArgProGlnIleLysAs 317
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------CCTGTGAGAACAACATCTCGCTCCCTGTTCTGTCCCGTCGA 1917
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268 rValAsnGlyGln---AlaLysThrHisThrGluAsnSerGlu-------
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Sequence 9, Application US/09291417D
GENERAL INFORMATION:
APPLICANT: WARTINEZ, RICARDO
APPLICANT: WHYTE, DAVID
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 038602/0329
CURRENT APPLICATION NUMBER: US/09/291,417D
CURRENT PILING DATE: 1999-04-13
PRIOR FILING DATE: 1998-04-14
NUMBER: OF SEQ ID NOS: 155
SOFTWARE: PATCHING DATE: 1998-04-14
NUMBER: OF SEQ ID NOS: 155
SOFTWARE: PATCHING DATE: 1998-04-14
NUMBER: OF SEQ ID NOS: 155
SOFTWARE: PATCHING DATE: 1998-04-14
NUMBER: OF SEQ ID NOS: 155
SEQ ID NO 9
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Matches:
Conservative:
Mismatches:
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ORGANISM: Homo sapiens
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170 ---GluArgLeuArgLeuGluGlnGlnLysGlnGlnIleMetAlaAlaLeuAsnSerGln 188
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                                                                                                                                                                                                                                  189 ThralaValGlnPheGlnGlnTyralaAlaGlnGlnTyrProGlyAsnTyrGluGlnGln
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APPLICANT: MARTINEZ, RICARDO
APPLICANT: WHYTE, DAVID
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
TITLE REPERNICE: 038602/0328
CURRENT APPLICATION NUMBER: US/09/688,188B
CURRENT FILING DATE: 12000-10-16
PRIOR FILING DATE: 1999-04-14
PRIOR PPLICATION NUMBER: 60/081,784
PRIOR PPLICATION NUMBER: 60/081,784
PRIOR PLING DATE: 1998-04-14
NUMBER: OF SEQ ID NOS: 155
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Matches:
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GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
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Patent No. 6514694

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: MILHAUSE, MICHAEL JAMES

TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THER FILE REFERENCE: TX-1-C2

CURRENT APPLICATION NUMBER: 1898-12-18

PRIOR APPLICATION NUMBER: 08/994,825

PRIOR FILING DATE: 1997-12-19
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                                         ------CAGGAGTATATCAGGCGACAGCTAGAAGAGGAGCAGCGGCACTTGGAAGTC 1332
                                                                                                                  1333 CTTCAGCAGCAGCTGCTCCAGGAGCAGGCCATGTTACTGCATGACCATAGGAGGCCGCAC 1392
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                 191 ValGlnPheGlnGlnTyrAlaAlaGlnGlnTyrProGlyAsnTyrGluGlnGlnGlnIle 210
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26.15%
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Query Match:
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LENGTH: 1835
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   NUMBER OF SEQ ID NOS: 155
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
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1633 CCCATCCCC 1641
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Best Local Similarity:
Query Match:
                                                                                 , ORGANISM: Homo
US-09-291-417D-11
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US-09-248-796A-7812
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Patent No. 6880170
GENERAL INFORMATION:
APPLICANT: PLOWANIN, GREGORY
APPLICANT: MAYTE, DAVID
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 038602/0329
CURRENT APPLICATION NUMBER: US/09/291,417D
CURRENT FILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-04-14
Conservative:
Mismatches:
Indels:
                                                                              US-09-762-594-7 (1-463) x US-09-688-188B-11 (1-4133)
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242 GlnGlnGluValValMetAlaGlyAlaSerLeuProAlaSerSerLysValAsnThrAla
                                                                      GlyAlaSerAspThrLeuSerValAsnGlyGlnAlaLysThrHisThrGluAsnSerGlu
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23, Application US/09520781
Fatent No. 6689866
GENERAL INFORMATION:
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
FILE REFERENCE: 1596-540 No. 668986681 Polynucleotides
CURRENT APPLICATION NUMBER: US/09/520,781
CURRENT PILING DATE: 2000-03-08
FRICE APPLICATION NUMBER: USSN 60/123,667
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US-09-520-781-23
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ORGANISM: Homo sapiens
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               GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT APPLICATION NUMBER: US/09/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 7812
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APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAY
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
PRIOR SEQIENCE ACID NOS: 28208
SEQIENT OF ACID NOS: 28208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     972 GAAAGGGAGCGACAÁAGAGCAGTTÁGAAAGGGAACÁGCTGGAATGGGAGAGAGAGÁGCGCAGA 1031
                                                                                                                                                    267 LeuSerValAsnGlyGlnAlaLysThrHisThrGluAsnSerGluLysValLeuGluPro 286
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                                                                                   153 GluGluAspArgieuArgArgGluGluGluGluArgArgArgIleGluGluGluArgieu 172
                                                                                                                                                                                                                     193 PheGlnGlnTyrAlaAlaGlnGlnTyrProGlyAsnTyrGluGlnGlnGlnIleLeuIle 212
                                                                                                                                                                                                                                                                                                                                                       232 ProAlaGlnGlnGlnAlaAlaLeuGlnLysGlnGln------GluValVal 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 MetAlaGlyAlaSerLeuProAlaSerSerLysValAsnThrAlaGlyAlaSerAspThr 266
                                                                  GlnArgGluGluGluGluArgGluArgLeuGlnLysGluGluGluLysArgLysArgGlu 152
                                                                                                                                                                                                173 ArgLeuGluGlnGlnLysGlnGlnIleMetAlaAlaLeuAsnSerGlnThrAlaValGln 192
                                                                                                                                                                                                                                                                                      213 ArgGlnLeuGlnGlu---GlnHisTyrGlnGlnTyrLysHisGlnAlaGluGlnThrGln 231
 SerHisArglleGluLysGluGluGluGluLysArgArgLysAlaGluGluGluArgArg
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Matches:
Conservative:
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; Patent No. 6747137
; GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
DB:
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US-09-248-796A-4611
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                                                                                                                                                                                                                                                                                                                                  286
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                  |||| :::!|||:::||| GAGAGAGAGAGAGAGAGAGAGAGAGAACGCTGGAG 875
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173 ArgLeuGluGlnGlnLysGlnGlnIleMetAlaAlaLeuAsnSerGlnThrAlaValGln 192
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                                                             PheGinGlnTyrAlaAlaGlnGlnTyrProGlyAsnTyrGluGlnGlnGlnIleLeuile
                                                                                 ArgGlnLeuGlnGlu---GlnHisTyrGlnGlnTyrLysHisGlnAlaGluGlnThrGln
                                                                                                                                                             912 CGGGAGGGCAAGAAAGACGAGAAGAGGAGGCTGGAGAGACTGGAACGGGAGAGGCAA
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Sequence 21, Application US/09520781

Sequence 21, Application US/09520781

Sequence 21, Application US/09520781

Sequence 21, Application US/09520781

SERENCE INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCOR TILE OF THE PETERENCE: 12966-540 No. 66898661 Polynucleotides

CURRENT APPLICATION NUMBER: US/09/520,781

CURRENT APPLICATION NUMBER: USN 60/123,667

PRIOR PILING DATE: 1999-03-09

NUMBER OF SEQ ID NOS: 81

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 21

LENGTH: 2010
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Mismatches:
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Matches:
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8.29%
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US-09-520-781-21
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ORGANISM: Homo sapiens
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Pred. No.:
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Sequence 1083, Application US/09949016
Betent No. 681239
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL THOROWATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1339 TTGGGAAATTGGTGGGAGGCTGCTGGTGCGAGCTTCTTAGGTGTTTACGGCAATCAAAGT 1398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 ArgargargGluTrpAlaAlaLeuGlyAsnMetSerLysGluAspAlaMetValGluPhe 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 AlaAlaLeuAsnSerGlnThrAlaValGlnPheGlnGlnTyrAlaAlaGlnGlnTyrPro
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Mismatches:
Indels:
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Matches:
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 1083
LENCTH: 3536
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                      AspArgLeuArgArgGluGluGluGluArgArgArgIleGluGluGluArgLeuArgLeu 174
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                                                            ArgileGluLysGluGluGluGluLysArgArgLysAlaGluGluGluArgArgGlnArg 134
                                                                                                 511 GCAAAG---AGATTGGAAGAGGAGGAACGTAAACGTAAAGGAGAAGAAGAAGCTAGAAAG 567
                                                                                                                                                                                                                                                                                                     GluGlnGlnLysGlnGlnIleMetAlaAlaLeuAsnSerGlnThrAlaValGlnPheGln 194
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                                                                                                                                                                    325 AspAlaAspSerVallleThrValArgArgGlyGluValValThrVal------
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                    US-09-762-594-7 (1-463) x US-09-248-796A-4611 (1-1542)
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CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS AN
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                                                                              1780 CTCCCCACTCGCATTGAAAAGTTTGACCGAAGCTCTTGGTTACGA---CAGGAAGAAGAC 1836
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   --TyrLysHisGlnAlaGluGlnThrGlnProAlaGlnGlnAlaAla 238
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                      239 LeuGlnLysGlnGlnGluValValMetAlaGlyAlaSerLeuProAlaSerSerLysVal
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/09425324A
Patent NO. 6562591
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: A-68344/RMS/DHR
CURRENT APPLICATION NUMBER: US/09/425,324A ·
CURRENT PILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
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ORGANISM: Artificial Sequence
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GlnGluValValMetAlaGlyAlaSerLeuProAla----SerSerLysValAsnThr 260
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                                                                              2371 CTGAATGTGACTGTGGACGTGCAGTCT---CCAGCTTGTACCTCATCTCCCATCACTCCG
                                                       261 AlaGlyAlaSerAspThrLeuSerValAsnGlyGlnAlaLysThrHisThrGluAsnSer
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Matches:
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                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVEL GERMINAL CENTER KIN, TITLE OF INVENTION: MCTHODS OF USE
TITLE OF INVENTION: MCTHODS OF USE
TITLE OF INVENTION: MCTHODS OF USE
CURRENT APPLICATION NUMBER: US/09/645,456A
CURRENT APPLICATION NUMBER: US/09/425,324
PRIOR PILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 36
SEQ ID NO 7
SEQ ID NO 7
                                                                                                                                               2488 GACGACTCCACCGATGAGGCC---
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Patent No. 6562580
GENERAL INFORMATION:
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US-09-645-456A-7
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1480 AAGCAAGAAAGAGACTACTTAGTTTCCCTTCAGCATCAGCGGCAGGAGCAGGAGCCTGTG 1539
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                      206 GluginGlnGlnIleLeuIleArgGlnLeuGlnGluGlnHisTyrGlnGln----- 222
                                                                           223 ------TyrLysHisGlnAlaGluGlnThrGlnProAlaGlnGlnGlnAlaAla 238
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Search completed: August 23, 2005, 00:08:12 Job time : 257 secs

Sequence 208, App Sequence 12147, A Sequence 17361, A Sequence 209, App

26802, A 11257, A 93, Appl 93, Appl 13424, A

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Title: Perfect score:

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Scoring table:

Searched:

Database

Sequence Sequence Sequence

5482709 5482709

Patent No. Patent No.

Sequence

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6.8%; Score 99.6; DB 1; Length 7218;
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Fatent No. 5670367
GENERAL INFORMATION:
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSER: Folse & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/232,463
                  5482709-5
5482709-5
US-08-78-891-208
US-09-618-166-208
US-09-949-016-12147
US-09-949-016-12147
US-09-949-016-1216-209
US-09-270-76-26802
US-09-270-767-11257
US-09-270-767-11257
US-09-949-016-13424
US-09-949-016-13424
US-09-949-016-17032
US-09-949-016-17033
US-09-949-016-17033
US-09-949-016-17033
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CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313

FILLING DATE: 4040-1991
ATTORNEY/AGENT INFORMATION:
NAME: BRYT, Stephen A.
REGISTRATION NUMBER: 29,768

REFERENCE/FOOCKET VINDER: 29,768

REFERENCE/FOOCKET VINDER: 30472/114 INMU
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 633-9300
TELEFRAX: (703) 683-4109
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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; CLONE: pT2gpt-F18
US-08-232-463-14
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                      STATE:
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16775, A 2, Appli 3, Appli 3, Appli 4, 
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8874.824 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
                  5.1.6
Compugen Ltd.
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US-09-298-568-1

US-09-894-273-1

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US-08-770-569A-20

US-08-770-569A-20

US-09-249-585A-2

US-09-949-016-1675-1

US-09-949-585A-2

US-09-160-189-3

US-09-10-199-3

US-09-150-114-1

US-09-647-344A-14

US-09-647-344A-14

US-09-647-344A-14

US-09-620-925-1

US-09-620-925-1

US-09-784-811-15

US-08-09-784-15
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PCT-US93-04648-15
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US-09-471-669A-48
                                                                                                                                                                                                                                                                                                                                                                                            1202784 seqs, 818138359 residues
                  GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                    - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                       IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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1459
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Match Length DB
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417 AAGAACGAGAGGGGCTGCAAAAGGAAGAAGAAGGGGAAGCGAAGGAGGAGGAAGACGGC 476
564 ACTCGCAGACTGCCGTGCAATTCCAGCAGTATGCAGCCCAGCAGTATCCAGGGAACTACG 623
                                                                          624 AACAACAGCAGATTCTCATCCGCCAGCTGCAGGAGCAGCACTATCAGCAGTATAAACACC
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                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Baseo, James J.
APPLICANT: Redelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Immediate Early Protein From Kaposi's
TITLE OF INVENTION: Encoding Same And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 74.2; DB 2; Length 3. Pred. No. 1.7e-10; 0; Mismatches 228; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08728323A Patent No. 5948676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 05:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.1%;
Best Local Similarity 50.3%;
Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 3489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
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US-08-728-323A-1
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APPLICANT: Kazemi-Esfarjani, Parsa
APPLICANT: Benzer, Seymour
TITLE OF INVENTION: AM ANIMAL MODEL OF POLYGLUTAMINE
TITLE OF INVENTION: TOXICITY, METHODS OF USE, AND MODULATORS OF POLYGLUTAMINE
TITLE OF INVENTION: TOXICITY
FILE REFERENCE: 06618-686001
CURRENT APPLICATION NUMBER: US/09/639,207
CURRENT FILING DATE: 2000-08-14
PRIOR FILING DATE: 1999-08-12
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                                                         226 GGGGAATGATAGGAGGAGAGAATGGGCAGCTCTGGGAAACATGTCCAAGGAGGATGCCAT 285
                                                                                                                                 GGTAGAGTTTGTGAAGCTTCTAAATAAGTGTTGTCCTCTCCTCTCGGCATATGTTGCGTC 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        384 AGGCGGAGGAGCGAAGGCAGCGTGAAGAGGAAGAACGAGAGGCGGCTGCAAAAGGAAG 443
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                                                                                                                                                                                                        GCGTGAAGAAGAACGAGAGCGGCTGCAAAAGGAAGAAGAAGAAGCGGAAGCGAGAGGGA
                                                                                                                                                                                                                                                                                                                                                            GGAAGACCGGCTGAGACGGAGGAGGAGAGAGGCGGCGGGATAGAGGAAGAGAGTTCG
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                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 171; Indels
2.6%; Pred. No. 1.3e-17;
tive 247; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: US 60/148,933
PRIOR FILING DATE: 1999-08-12
PRIOR FILING DATE: 1999-08-12
PRIOR FILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 60/177,047
PRIOR APPLICATION NUMBER: US 60/205,720
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 69
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FastSEQ for Windows Version 4.0
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Patent No. 6815575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Synthetic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 51.44
Matches 181; Conservative
                   Conservative
 Best Local Similarity
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SEQ ID NO 13
                                                                                                                                 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or Enhance the Binding of Viral DNA
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                                                                   AGGAGCACTATCAGCAGTATAAACACCAG--GCAGAGCAAACCCAACCTGCACAACA
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Pred. No. 1.7e-10;
0; Mismatches 228; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or E:
TITLE OF INVENTION: to Genomic Host DNA
FILE REFERENCE: UM-03778
CURRENT APPLICATION NUMBER: US/09/410,399
CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09410399; Patent No. 6482587; GENERAL INFORMATION:
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Best Local Similarity 50.3%;
Matches 236; Conservative
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APPLICANT: Kieff, Elliott D.
APPLICANT: Ballestas, Mary B.
APPLICANT: Ballestas, Mary B.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE FILE REPRENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US 60/109,422
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER PILING DATE: 1998-11-19
SOFTWARE: PALENTIN DOS: 3
SOFTWARE: PALENTIN VOS: 2.0
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Patent No. 6322792
GENERAL INFORMATION:
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                                                             APPLICANT: Kieff, Elliott D.
APPLICANT: Kafef, Elliott D.
APPLICANT: Ballestas, Mary E.
APPLICANT: Raye, Kenneth M.
TITLE OF INVENTION: HANDINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE FILE REFERENCE: 16412-1001R
CURRENT APPLICATION NUMBER: US/09/894,273
PRIOR APPLICATION NUMBER: US 60/109,422
PRIOR FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
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APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: POLYPETIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.1%; Score 74.2; DB 4; Length 3489; 50.3%; Pred. No. 1.7e-10; Live 0; Mismatches 228; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
, ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-894-273-1
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Sequence 1, Application US/09894273
Patent No. 6756203
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 50.3<sup>†</sup>
Matches 236; Conservative
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                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,379
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.1%; Score 74.2; DB 2; 50.3%; Pred. No. 6.7e-10;
Dunham LLP
of the Americas
                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52342
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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Cooper &
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                         1185 Avenue
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US-08-757-669A-20/c
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Score 74.2; DB 3;
Pred. No. 6.7e-10;
0; Mismatches 228;
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US-09-230-371A-20
                                                                                                     Sequence 20, Application US/09230371A; Patent No. 6348586; GENERAL INFORMATION:
                                                                                                                                                                                   APPLICANT: Bohenzky, Roy A
APPLICANT: Russo, James J
APPLICANT: Edelman, Islance S
APPLICANT: Moore, Patrick S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.1%;
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SOFTWARE: Patentin Ver. 2.0
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Bohenzky, Roy A
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US-09-949-016-16775/c
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Best Local 8
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                     APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Edelman, Isidore S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS TITLE OF INVENTION: SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 20
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,669A
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Pred. No. 6.7e-10;
0; Mismatches 228;
                                                                                                                                                              ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
ATTORNEY/AGART INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45185-F
TELECOMMUNICATION:
TELECHONE: (212) 2705-0400
                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
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           Bohenzky, Roy A.
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Best Local Similarity 50.3%;
Matches 236; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper &
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MEDIUM TYPE: Floppy
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TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND TITLE OF INVENTION: USES THEREOF FILE REFERENCE: 45.185-G-PCT-US CURRENT APPLICATION NUMBER: US/09/230,371A PRIOR PILING DATE: 1999-11-17 PRIOR FILING DATE: 1997-07-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            537 AAAAGCAGCAGCAGATTAAACTCGCAGACTGCCGTGCAATTCCAGCAGTATG 596
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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
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SOFTWARE: Pate
SEQ ID NO 3
LENGTH: 1926
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US-09-410-399-3
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Best Local S:
Matches 195
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PELICATION NUMBER: 60/237,768
PRIOR PELICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PELICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
SOFTWARE: FREESEQ for Windows Version 4.0
SEC ID NO 16/775
LENGTH: 12695
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APPLICANT: HOTLICK, Robert
TILLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
FILLE REPERENCE: 0867/05095
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILLING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
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Pred. No. 5.6e-10;
0; Mismatches 209;
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OTHER INFORMATION: coding strand of EBNA-1 DNA
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Patent No. 6417002
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llarity 48.8%;
Conservative
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ORGANISM: Epstein Barr Virus
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Best Local Similarity
Matches 199; Conser
                                                                                                                                                                                                                Human
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NAME/KEY: CDS
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US-09-249-585A-2
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Length 1926;
Score 72.6; DB 3; Length 1 Pred. No. 3.4e-10; 0; Mismatches 204; Indels
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APPLICANT: Robertson, Erle S.
TITLE OF INVENTION: Methods to Inhibit or E.
TITLE OF INVENTION: Methods to Inhibit or E.
TITLE REFERENCE: UN-03778
CURRENT APPLICATION NUMBER: US/09/410,399; CURRENT FILING DATE: 1999-10-01
5.0%;
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US-09-410-399-3
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Query Match
Best Local Similarity 48.9°
Matches 195; Conservative
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ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
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48.9%; Pred. No. 4.1e-10;
ive 0; Mismatches 204; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS
TELECOMMUNICATION:
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FILING DATE: 22-Jul-1999
CLASSIFICATION: <Unknown>
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APPLICATION NUMBER: 09/050,863
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INPORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO:
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(415) 949-8711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Patent No. 6316223.
GENERAL INFORMATION:
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STRANDEDNESS: unknown
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Payan, Don
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Best Local Similarity 48.9 Matches 195; Conservative
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                                                        749 CAGGAGGGCÁGGAGCAGGAGGGCAGGÁGGGGCÁGGÁGGAGGAGGAGGAGGAGGAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Lao, Ying
APPLICANT: Hiang, Betty
APPLICANT: Payan, Don
TITLE OF INVENTION: Mammalian Protein Interaction Cloning
TITLE OF INVENTION: System
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                             754
                                                                                                                                                                                                                                                                                                   GAGGGGAGGGGCAGCAGCAGGAGGGCAGGAGGGG 907
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SOPTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,863
                                                                                                                                                                                                                                       716 GCAGCATTACAGAAACAGCAAGAAGTAGTGATGGCTGGG
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Pred. No. 4.1e-10;
0; Mismatches 204;
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NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS
TELECOMMUNICATION INPORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09050863
Patent No. 6114111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: Floppy disk
IBM PC compatible
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2580 base pairs
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Matches 195; Conservative
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STRANDEDNESS: unkno
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                           476 CTGAGACGGGAGGAGGAGGAGGCGGCGGATAGAGGAAGAGGCTTCGGCTGGAACAG
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Patent No. 5976807

GENERAL INFORMATION:

APPLICANT: Horlick, Robert A.

APPLICANT: Bonaj, Bassam B.

APPLICANT: Robbins, Alan K.

TILLE OF INVENTION: Extravotic Cells Stably Expressing Genes

TILLE OF INVENTION: Example Transfected Episomes

FILE REFERENCE: 0867/1D903US1

CURRENT APPLICATION NUMBER: US/09/130,114

CURRENT FILING DATE: 1998-08-06

NUMBER OF SEQ ID NOS: 36

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.0%; Score 72.6; DB 2; Length 5452;
48.9%; Pred. No. 6.5e-10;
tive 0; Mismatches 204; Indels 0
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Best Local Similarity 48.94
Matches 195; Conservative
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Perfect score:

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Sequence 327, App
Sequence 33, Appl
Sequence 136, Ap
Sequence 13381, A
Sequence 265, Ap
Sequence 265, Appl
Sequence 18, Appl
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Sequence 21, Appl
Sequence 21, Appl
Sequence 7048, Appl
Sequence 15, Appl
Sequence 16, Appl
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Sequence 61, Appl
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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APPLICANT: LAL, Preet,
APPLICANT: LAL, Preet,
APPLICANT: TANG, Y. Tom
APPLICANT: CORLEY, Neil C.
APPLICANT: GURGLER, Karl J.
APPLICANT: GURGLER, Karl J.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: PATTERSON, Chandra
TITLE OF INVENTION: NEUROTRANSMISSION ASSOCIATED PROTEINS
FILE REFERENCE: PF-0551 PCT
                                                                                                                                                                                                                                                                                                                                                        US-09-864-761-13381
US-09-864-761-13381
US-09-90-133-265
US-09-90-141-9
US-09-90-141-9
US-10-725-121-9
US-10-725-121-9
US-10-725-121-9
US-10-494-940-21
US-10-494-940-21
US-10-934-998-284
US-10-934-998-284
US-10-934-998-284
US-10-934-998-15
US-10-820-583A-15
US-10-820-583A-15
US-10-820-583A-17
US-10-840-512-91
US-09-789-390-36
US-09-789-390-36
US-09-789-390-36
US-10-425-114-9663
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US-10-723-860-1746
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                                                                         SUMMARIES
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-MODEL=frame+ p2n.model -DEV=xlh
-Q0=/Cgn2 1/USFTO_spool/US09762594/runat_19082005_171347_18277/app_query.fasta_1.647
-Q3=/Cgn2 1/USFTO_spool/US09762594/runat_19082005_171347_18277/app_query.fasta_1.647
-DB=Published Applications NA -OFMT=fastap -SUFFIX=rnpb -MINNATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bite -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORES=pct -THR MAXELEN=10.0
-THR MIN-0 -ALIGN=15 -MODE=LOCAL -OUTFFT-pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=2000000000 -USER=US09762594 @CGN 1 1_480 @runat_19082005_171347_18277
-NCPUG-6 -IPCUP-3 -NO MAAP -LARGEQUERY -NGS GORRS=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOTT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPDEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                  August 22, 2005, 22:38:38; Search time 882 Seconds (without alignments) 3410.514 Million cell updates/sec
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(cgn2_6/ptodata12/pubpna/USO7_NEW_PUB.seq:+
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(cgn2_6/ptodata12/pubpna/USO0P_PUBCOMB.seq:+
(cgn2_6/ptodata12/pubpna/USOOP_PUBCOMB.seq:+
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/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:
                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                 OM protein - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7316285 segs, 3248459403 residues
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Maximum Match 100%
Listing first 45 summaries
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Ygapext
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Maximum DB seq length: 2000000000
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Ygapop 10.0 , Y
Fgapop 6.0 , F
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Database

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1274 CAATATCCAGGGGGGGGGGCTATCTCCTCAAGTTTGACAACTCCTACTTTGTGGGGG 1333
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    734 TTGCCTACATCATCAAAAGTGAATGCAACTGTACCAAGTAATATGATGTCAGTTAATGGA 793
                                                                                       914 CGACCTCAGATCAAAGACTTCAAAGAGAGATTCAGCAGGATGCAGATTCCGTGATTACA
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                                 GlnAlaLysThrHisThrGluAsnSerGluLysValLeuGluProGluAlaAlaGluGlu
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Publication No. US20040044181A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

TITLE REFREENCE: 21272-113 (793)

CURRENT APPLICATION NUMBER: US/10/363,616

CURRENT FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: 09/654,935

PRIOR PILING DATE: 2000-09-01

SEQ. ID NO 238
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Mismatches:
Indels:
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ORGANISM: Homo sapiens
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US-10-363-616-238
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Query Match:
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Matches:
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Indels:
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CURRENT APPLICATION NUMBER: US/10/998,342
CURRENT FILING DATE: 2004-11-29
FRIOR APPLICATION NUMBER: US/09/720,530
FRIOR FILING DATE: 2000-12-19
FRIOR PILING DATE: 2000-12-19
FRIOR FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PERL Program
SOFTWARE: PERL Program
LENGTH: 1481
                                                                                                                                                                                        NAME/KEY: misc_feature
OTHER INFORMATION: Incyte Clone No: 998868
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2021.00
94.21%
89.12%
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304 IlealaalaproSerMetTrpThrargProGlnIleLysAspPheLysGluLysIleArg 323
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| GACATCGTTATGATC-----CAGTCTGAACATACAGGAGGT
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                  Indels:
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SEQ ID NO 932
LENGTH: 3547
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ORGANISM: Homo sapiens
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                                 TCTGCAGATCTTCTGGGGGACCACAGGAAAGTCTCCCCACCTCTGATGGCTCCTCCATGC
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                                                                        GlnPheGlnGlnTyrAlaAlaGlnGlnTyrProGlyAsnTyrGluGlnGlnGlnIleLeu
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Publication No. US20040005560A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
FILE REFERENCE: H1-A0106
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Patent No. US20020009758A1
| GENERAL INPORMATION:
| APPLICANT: Harlocker, Susan L.
| APPLICANT: Hang, Tongtong
| APPLICANT: Bangur, Chaitanya S.
| APPLICANT: Switzer, Anne
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
| TITLE OF INVENTION: ADD DIAGNOSIS OF LUNG CANCER.
| FILE REFERENCE: 21012.502
| CURRENT PAPLICATION NUMBER: US/09/866,562
| CURRENT FILING DATE: 2001-05-25
| SEQ ID NO 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 TCCGTCTACTACAGAGTCTATTATACTAGA 68
      Sequence 327, Application US/10469285
Publication No. US20040126776A1
GENERAL INFORMATION:
APPLICANT: LION Bioscience AG
TITLE OF INVENTION: Gene library
FILE REPERBNEE: L 1541
CURRENT APPLICATION NUMBER: US/10/469,285;
CURRENT FILING DATE: 2003-08-28
NUMBER OF SEQ ID NOS: 840
SOFTWARE: Petentin version 3:0
SOFTWARE: Petentin version 3:0
LENGTH: 278
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352.00
93.75%
87.50%
14.70%
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384.00
100.00%
100.00%
16.04%
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; ORGANISM: Mus Musculus
US-10-469-285-327
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US-09-866-562-33
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Best Local Similarity:
Query Match:
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Best Local Similarity:
US-10-469-285-327/c
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Pred. No.:
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US-10-72-860-1746/

Sequence 1746, Application US/10723860

; Publication No. US20040253606A1

; GENERAL INFORMATION:

APPLICANT: Aziz, Natasha

; APPLICANT: Zlotnik, Albert

; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &

; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators

; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators

; FILE REFERENCE: 05882.0193 nPUS01

; CURRENT APPLICATION NUMBER: US/10/723,860

; CURRENT FILING DATE: 2003-11-26

; PRIOR PILING DATE: 2003-11-26

; WIMBER OF SEQ ID NOS: 8393

; SOFTWARE: PatentIn version 3.2
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                                                                        266 -----ThrLeuSerValAsnGlyGlnAlaLysThrHisThrGluAsn-----
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Matches:
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US-09-762-594-7 (1-463) x US-09-866-562-33 (1-934)
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Best Local Similarity:
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LENGTH: 210204
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Sequence 30285, Application US/09864761
Sequence 30285, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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EXPRESSED IN PACKENTA, SIGNAL = 1.6
EXPRESSED IN BONE MARROW, SIGNAL = 1.6
EXPRESSED IN FUNG, SIGNAL = 2.4
EXPRESSED IN LING, SIGNAL = 2.4
EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR PRICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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ORGANISM: Homo sapiens
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APPLICANT: Penn, Sharron G.

APPLICANT: Penn, Sharron G.

APPLICANT: Penn, Sharron G.

APPLICANT: Penn, Sharron G.

APPLICANT: Hanzel, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMBER SERSSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION: HUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2000-02-03

PRIOR PAPLICATION NUMBER: US 60/180,312

PRIOR PAPLICATION NUMBER: US 60/207,456

PRIOR PAPLICATION NUMBER: US 60/207,456

PRIOR PAPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-08-03

PRIOR PAPLICATION NUMBER: US 60/203,366

PRIOR FILING DATE: 2000-00-08-03

PRIOR PAPLICATION NUMBER: PCT/US01/00666

PRIOR PAPLICATION NUMBER: PCT/US01/00667

PRIOR PAPLICATION NUMBER: PCT/US01/00667

PRIOR PAPLICATION NUMBER: PCT/US01/00669

PRIOR PLING DATE: 2001-01-30

PRIOR PLING D
  130550 TCTGACTGTGCCAGCCTCTCTTAGCAAAATGCCCGGGGTACTCATGTTTCCTCATGGTTT 130491
                                                                                                                 -----GICCTTCAGICTCCCCA--- 130455
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                                                         ---SerGluLysValLeuGluProGluAlaAlaGluGluAlaLeuGluAsnGlyProLys
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
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Patent No. US20020048763A1
GENERAL INFORMATION:
                                                                                      130490 CTCAGTGCTAAGCTGCTT----
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340 ValArgValProThrHisGluGluGlySerTyrLeuPheTrpGluPheAlaThrAspSer 359
                                      360 TyrAspileGlyPheGlyValTyrPheGluTrpThrAspSerProAsnAlaAlaValSer 379
                                                                                                                                                                  138 GluArgGluArgLeuGlnLysGluGluGlu---LysArgLysArgGluGluGluAspArg
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APPLICANT: GRIPS, MARTIN
APPLICANT: GCHMITZ, ANNE-CHANTAL
APPLICANT: SCHMITZ, ANNE-CHANTAL
APPLICANT: SERS, CHRISTINS
TITLE OF INVENTION: DETECTION OF DIFFERENTIAL GENE EXPRESSIONS
TITLE OF INVENTION NUMBER: US/09/930,213
CURRENT FILING DATE: 2001-01-31
PRIOR PLICATION NUMBER: DE 10004102.7
PRIOR APPLICATION NUMBER: DE 10004102.7
PRIOR PRIME OF SEQ ID NOS: 885
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 265
                                                                                                                                                                                                                                                               380 ValHisValSerGluSerSerAspGluGluGluGluGluGluGlu
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Publication No. US20030170625A1
GENERAL INFORMATION:
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US-09-930-213-265
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N: EXPRESSED IN BLACENTA, SIGNAL = 1.8

N: EXPRESSED IN BONE WARROW, SIGNAL = 1.6

N: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6

N: EXPRESSED IN LUNG, SIGNAL = 2.4

N: EXPRESSED IN LUNG, SIGNAL = 1.7

N: EXPRESSED IN HELA, SIGNAL = 1.7

N: EXPRESSED IN HELA, SIGNAL = 1.7

N: THI: AF022770.2, EVALUE 3.00e-03

N: SWISSPROT HIT: P49193, EVALUE 1.30e-01

N: EST_HUMAN HIT: A8292776.1, EVALUE 0.00e+00
          PRIOR FILING DATE: 2000-02-04

PRIOR FILING DATE: 2000-05-26

PRIOR PRILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-06-03

PRIOR FILING DATE: 2000-06-03

PRIOR FILING DATE: 2000-00-03

PRIOR FILING DATE: 2000-00-07

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR PRILING DATE: 2001-01-03

PRIOR FILING DATE: 2001-01-30

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PRIOR PRIOR PRICATION NUMBER: US 09/774, 203

PRIOR FILING DATE: 2001-01-30

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                                                                                                                                                                                                                                                                                                               115 ArgileGluLysGluGluGluLysArgArgLysAlgLuGluGluGluArgArgGlnArg
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Mismatches:
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Matches:
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                                                                                                           9.28e-13
229.00
48.45%
29.46%
9.57%
                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
                   TYPE: DNA
ORGANISM: HUMAN
 ; LENGTH: 3792
; TYPE: DNA
; ORGANISM: HUMAU
US-10-820-583A-18
                                                                                             Alignment Scores:
LENGTH: 3792
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1892 TTAGAGGAGAACCGGCTGCGGATGGAAGAGGAGGCAGCCAGACTCCCGGCATGAGGAAGAA 1951
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                                                                                                                           1952 GAACGGAAGAGAAAGGAGCTGGAGGTCCAGCGGCAGAAGGAGTTAATGCGCCAGAGGCAG 2011
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2251 ACAGCAACAGCAGAAACTCTCAGGTTGGGGGAATGTCAGCAAACCTTCAGGTACCACGAA 2310
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                                                                                           -----ThrGlnProAla 233
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               --GlnTyrLysHisGlnAlaGlu
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Publication No. US20040242461A1
GENERAL INFORMATION:
APPLICANT: Schneider, Michael
APPLICANT: Oh. Hidemasa
TITLE OF INVENTION: Modulators of Telomere Stability
FILE REFERENCE: HO-PO2673US1
CURRENT APPLICATION NUMBER: US/10/820,583A
CURRENT FILING DATE: 2004-04-08
PRIOR FILING DATE: 2003-04-08
PRIOR FILING DATE: 2003-04-08
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 18
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           LeuGlnGluGlnHisTyrGln-
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                                      1876 -----CCTGTGAGAACAACATCTCGCTCCCCTGTTCTGTCCGGTCGA 1917
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                     317 pPheLysGluLysIleArgGlnAspAlaAspSerValIleThrValArgArg
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                                                                                                 Sequence 9, Application US/10725329; Sequence 9, Application US/10725329; Publication No. US200402243231
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: MHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES; FILE REPRENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/10/725,329
; CURRENT FILING DATE: 2000-10-16
; PRIOR FILING DATE: 2000-10-16
; PRIOR FILING DATE: 1999-04-14
; PRIOR FILING DATE: 1999-04-14
; PRIOR FILING DATE: 1999-04-14
; RIGHT PARTING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE PARENTIN VET. 2.1
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Matches:
Conservative:
Mismatches:
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ORGANISM: Homo sapiens
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Best Local Similarity:
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APPLICANT: MARTINEZ, RICARDO
HITLE OF INVENTION STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 240/300
CURRENT APPLICATION NUMBER: US/09/291,417A
CURRENT FILING DATE: 1999-04-13
EARLIER FILING DATE: 1999-04-14
SARLIER FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PSESEQ for Windows Version 3.0
SEQ ID NO 9
LENGTH: 3798
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Matches:
Conservative:
Mismatches:
Indels:
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229.00
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1438 CACTYGGAAGTCCTTCAGGACGACCTCGGACGACGACTAGTTACTCGGACGACTACTAGGACGACTACTCGGACGACCTACTACGACGACCTACTCGGACGACCTACTACCACGACGACCTACCT	Alignment Scores: Pred. No.: 228.50 Score: Score: A6.81\$ Conservative: 59 Best Local Similarity: 28.88 Mismatches: 9.54\$ Indels: BB: A12 Matches: A6.81\$ Mismatches: B1 DB: A28.88 Mismatches: A13
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Publication No. US20030194721A1
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2892 TTAGAGGAGAACCGGCTGCGGATGGAAGAGGAGGCAGCCAGACTCCGGCATGAGGAAGAA 2951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----TTGGGCTCTAT 3457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              328 erVallleThrValArgArgGlyGluValValThrValArgValProThr-HisGluGlu 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 GlySerTyrLeuPheTrpGluPheAlaThrAspSerTyrAspIleGlyPheGlyValTyr 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195 GlnTyrAlaAlaGlnGlnTyrProGlyAsnTyrGluGlnGlnGlnIleLeuIleArgGln 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuGlnGluGlnHisTyrGln------GlnTyrLysHisGlnAlaGlu 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 GinGinGlnAlaAlaLeu-----GinLysGlnGlnGlnValValMetAlaGly 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 GluGlnGlnLysGlnGlnIleMetAlaAlaLeuAsnSerGlnThrAlaValGlnPheGln 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----ThrGlnProAla 233
                                                                                                                                                                                                                                                                                                                              261 GAACTTGCCCGAAGGAAACAGGAAGAGGCTCTGCGTCGCCAGCGGGAGCAAGAATTGCA
                                                                                                                                                                                                                                                                         GluArgGluArgLeuGlnLysGluGluGlu---LysArgLysArgGluGluAspArg
                                                                                                                                                                                                SerGluLysValLeuGluPro---GluAlaAlaGluGlu-AlaLeuGluAsnGlyProLy
                                                                                                                                                                 ------ArgArgLysAlaGluGluGluArgArgGlnArgGluGluGlu
                                                                                                          LeuArg-----ArgGluGluGluArgArgArgIleGluGluGluArgLeuArgLeu
  US-09-762-594-7 (1-463) x US-10-494-940-21 (1-3612)
                                                       AlaSerHisArgIleGluLysGluGluGluLys
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US-10-247-671-58
; Sequence 58, Application US/10247671
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151 ArgGluGluGluAspArgLeuArgArgGluGluGluGluArgArgArgIleGluGluGlu 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glu------GluGluGluGluArgGluArgLeuGlnLysGluGluGluLysArgLys 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 ArgLeuArgLeuGluGlnGlnLysGlnGlnIleMetAlaAlaLeuAsnSerGlnThrAla 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 LeulleArgGln---LeuGlnGluGlnHisTyrGlnGlnTyrLysHisGlnAlaGluGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191 ValGlnPheGlnGlnTyrAlaAlaGlnGlnTyrProGlyAsnTyrGluGlnGlnGlnIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 ThrGlnProAlaGlnGlnGlnAlaAlaLeuGlnLysGlnGlnGluValValMetAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1511 PAGAGGAGAGTTGAAAGAGAA-------
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APPLICANT: Mikita, Thomas
APPLICANT: Mikita, Thomas
APPLICANT: Shiffman, Dov
APPLICANT: Porter, Gordon, J.
APPLICANT: Raser, Matchew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
FILE REFERENCE: PA-0050 US
CURRENT APPLICATION NUMBER: US/10/247,671
CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: 60/323,784
PRIOR PILING DATE: 2001-09-19
NUMBER OF SEO ID NOS: 186
SOFTWARE: PERL PROGram
SEO ID NO S8
LENGTH: 3925
                                                                                                                                                                                                                                                                                                                                                                  ) NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030194721A1 4436929CB1
US-10-247-671-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3925
71
46
76
43
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Mismatches:
Indels:
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226.50
49.58%
30.08%
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ORGANISM: Homo sapiens
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Best Local Similarity:
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QQ	1916CCTGTGAGAACAACAACTCTCGCTCCCGTCCGTCGA 1957
Search Job ti	Search completed: August 23, 2005, 02:22:57 Job time : 982 secs

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1459
1 gaattcgcggccgcgtcgac......catgacgtttaatttccttt 1459
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
4:: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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17: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/U
                           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                               - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 9, Appli Sequence 327, App Sequence 33, Appl Sequence 832, App Sequence 238, App Sequence 32, Appl Sequence 13381, A
SUMMARIES	21 US-10-998-342-9 19 US-10-469-285-327 9 US-09-866-562-33 17 US-10-108-260A-832 18 US-10-363-616-238 9 US-09-866-562-32 9 US-09-866-562-32
DB	21 17 17 18 18
Si Query re Match Length DB ID	1481 278 934 3547 882 527 554
% Query Match	73.6 18.4 14.0 10.3 7.8
Score	1073.2 268.2 204.4 150.8 150 113.4
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RESULT 1 US-10-998-342-9 Sequence 9, Application US/10998342 PUDICATION NO. US20050106672A1 GENERAL INFORMATION: APPLICANT: LAL, Freet, APPLICANT: LAL, Freet APPLICANT: CALLEY, Neil CALL APPLICANT: CORLEY, Neil C. APPLICANT: CORLEY, Neil C. APPLICANT: CORLEY, Neil C. APPLICANT: GORGONE, Gina A. APPLICANT: BAUGHN, MATIAR N. APPLICANT: GORGONE, GINA A. APPLICANT: BAUGHN, MATIAR N. APPLICANT: BAUGHN, MATIAR N. APPLICANT: DATTERSON, CHANGER: US/10/90000000000000000000000000000000000	ILT 1 10-998-342- gquence 9, gquence 9, blicaturing RPLICANT: RRICR RPLIN RRICR RPLIN RRICR APPLI RRICR RPLIN RRICR RILI RRICR RRICR RILI RRICR R	-9 APPlic NNO. UNCYII INCYII TALA, TANG, T	cation 1820050 1820050 1820050 1820050 182005 182005 182006 18200	ication US/1099834 US20050106672A1 UON: FE PHARMACEUTICALS Freet,	1099 72A1 72A1 7. 07 7. 07 7. 08 7. 08 7. 08 7. 08 7. 08 7. 08	LIGNMENTS INC. INC. 198,342 5,530	PROTEINS		

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                                                  CCACCAGTATCCAGGGAGGGGAGTCTATCTCCTCAAGTTTGATAATTCCTACTCTGTG
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TITLE OF INVENTION: Gene library
FILE REFERENCE: L 1541
CURRENT APPLICATION NUMBER: US/10/469,285
CURRENT FILING DATE: 2003-08-28
NUMBER OF SEQ ID NOS: 840
SOFTWARE: PATENTIN VETSION 3.0
SEQ ID NO 327
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US-09-866-562-33
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Matches 270; Conserv
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                                              73.6%; Score 1073.2; DB 21; Length 1481;
86.9%; Pred. No. 9.6e-307;
ive 0; Mismatches 178; Indels 0;
OTHER INFORMATION: Incyte Clone No: 998868
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Matches 1180; Conserv
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US-10-998-342-9
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                                                                                                                615 GTGACCATCCGGGTACCTACTCATCCAGAGGGGAAGCGTGTCTGCTGGGAGTTTGCGACC
                                                                                                                                                                                                                                                                                                                                    1139 GTCAGTGTGCATGTCAGTGAGTCCAGTGAGGAGGAGGAGGAGGAGGAAAATGTC---
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Pred. No. 3.1e-33;
0; Mismatches 195; Indels
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-113 (793)
CURRENT APPLICATION NUMBER: US/10/363,616
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 09/654,935
PRIOR PILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 238, Application US/10363616; Publication No. US20040044181A1; GENERAL INFORMATION:
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Best Local Similarity 57.8%;
Matches 304; Conservative
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SEQ ID NO 238
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ORGANISM: Homo sapiens
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; LOCATION: (109) .. (882)
US-10-363-616-238
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US-10-363-616-238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITAAAGAAGAATCGGCAGGATGCAGATTCTGTGATTACAGTACGTCGAGGAGAGTC 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1218 AGAACGCCAACAACACCTCTGCTGGATGAGATTGTACCTGTGTACCGGCGGGGACTGTCACG 1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        614
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Pred. No. 4e-33;
0; Mismatches 197; Indels 27; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 934;
                                                      APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Klee, Jennifer
APPLICANT: Klee, Jennifer
APPLICANT: Switzer, Anne
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER.
FILE REFERENCE: 210121.502
CURRENT APPLICATION NUMBER: US/09/866,562
CURRENT FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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TITLE OF INVENTION: No. US20040005560Alel full length cDNA
FILE REPERENCE: H1-A0106
CURRENT PAPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
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Pred. No. 2.4e-49;
2; Mismatches 43;
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Best Local Similarity 84.2%;
Matches 251; Conservative
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Best Local Similarity 57.7%;
Matches 306; Conservative
US20020009758A1
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US-09-866-562-33
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CORGANISM: Homo sapiens
US-10-108-260A-832
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US-10-108-260A-832
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1021 CACCGTCCGAGTCCCGACTCATGAGGATCATACCTATTTTGGGAATTTGCCACAGA 1080
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COTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9

COTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7

US-09-864-761-13381
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   GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 13381
                         FILE REFERENCE: Aeomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
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Best Local Similarity 61.1%;
Matches 179; Conservative (
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ORGANISM: Homo sapiens
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1364
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                                                                                                                                                                                                                       1232 CCTCTGCTGGATGAGATTGTACCTGTGTACCGGCGGGACTGTCACGAGGAAGTATATGCA 1291
                                                                                                                                                                                                                                                                                                                                             GGCAGCCACCAGTATCCAGGGGGGGGGGGTCTATCTCCTCAAGTTTGATAATTCCTACTCT 1351
                                                                                                ---TCACTTGTGAAGAAAGCAAAAAGAACGCCAACAAG 1231
61 AATCAGTCTACTACAGAGTCTATTATACTAGATAAAAATGTNGGTACAAAGTCTGGAGTC 120
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                                                                                                                                                                                                                                                             775 GGCAGCCATGACTACCTAGTGAGGCATCTACCTGCTCAAGTTCGACAACTCCTACTACC
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84.0%; Pred. No. 1.6e-22;
tive 0; Mismatches 24; Indels 0
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APPLICANT: Harlocker, Susan L.
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Klee, Jennifer
APPLICANT: Switzer, Anne
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER.
FILE REFERENCE: 210121.502
CURRENT APPLICATION NUMBER: US/09/866,562
CURRENT FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 96
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Patent No. US20020009758A1
GENERAL INFORMATION:
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OTHER INFORMATION: n = A,T,C or
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ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
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Best Local Similarity
Matches 126; Conserv
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LENGTH: 527
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N: EXPRESSED IN BLACENTA, SIGNAL = 1.8
N: EXPRESSED IN BONE MARKOW, SIGNAL = 1.6
N: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
N: EXPRESSED IN LUNG, SIGNAL = 2.4
N: EXPRESSED IN LUNG, SIGNAL = 2.4
N: EXPRESSED IN HELA, SIGNAL = 1.7
N: N: TIT AF022770.2, EVALUE 3.00e-03
N: SMISSPROT HIT: P49193, EVALUE 1.30e-01
N: EST_HUMAN HIT: A4292776.1, EVALUE 0.00e+00
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ive 0; Mismatches 113; Indels
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R FILING DATE: 2001-01-30
R APPLICATION NUMBER: PCT/USO1/00661
R FILING DATE: 2001-01-30
R FILING DATE: 2001-01-30
R FILING DATE: 2001-01-30
R APPLICATION NUMBER: PCT/USO1/00670
R APPLICATION NUMBER: US 60/234,687
                                                                                                                                              APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/USO1/00666
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00666
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
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APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00668
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APPLICATION NUMBER: PCT/US01/00663
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                                        FILING DATE: 2000-05-26
APPLICATION NUMBER: US 09/632,3
FILING DATE: 2000-08-03
APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-05-26
PRIOR PELICATION NUMBER: US 09/
PRIOR PELICATION NUMBER: GB 242
PRIOR PELICATION NUMBER: GB 242
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/US
PRIOR PELICATION NUMBER: PCT/US
PRIOR APPLICATION NUMBER: PCT/US
PRIOR APPLICATION NUMBER: PCT/US
PRIOR PILING DATE: 2001-01-30
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Matches 177; Conservative
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APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Acomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Aziz, Natasha
APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Ginsburg, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions of TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: 108/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR PRILING DATE: 2002-11-26
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         1081 CAGTTATGACATTGGGGTTTGGTTTATTTTGAATGGACAGACTCTCCAAATGCTGCTGT 1140
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                                                             303 TGACTATGACATTGGCTTTGGAGTTTATTTTGACTGGACCCCTGTAACTAGCACTGACAT
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61.1%; Pred. No. 3.7e-20;
tive 0; Mismatches 114;
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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                                                                                                                                                                                                                                                                                                                              Sequence 1746, Application US/10723860
Publication No. US20040253606A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 179; Conserv
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Sequence 13, Application US/10465217
Publication No. US20030204859A1
Publication No. US20030204859A1
GENERAL INFORMATION:
APPLICANT: Kazemi-Esfarjani, Parsa
APPLICANT: Benzer, Seymour
TITLE OF INVENTION: AN ANIMAL MODEL OF POLYGLUTAMINE
TITLE OF INVENTION: TOXICITY
TITLE OF INVENTION: TOXICITY
TITLE OF INVENTION: TOXICITY
CITLE OF INVENTION: USXICITY
CURRENT APPLICATION NUMBER: US/10/465,217
CURRENT FILING DATE: 2003-06-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                783 ACACAGCTGGAGCAAGTGATACACTGTCAGTTAATGGACAGGCCAAAAACCCACACTGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 595 GCTCCGAAAAMGAACTGGAACCAGAAGCTGCAGAAGAAGAAGAAAAAGGAGAAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  723 TACAGAAACAGCAAGAAGTAGTGGTGGCTGGGGCATCATTGCCTGCATCATCAAAGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     711 TCCAGAACCACCAGGAAGTAGT--AGGGCTGGTTTTCCTTGCCTACATCATCAAAAGTGA
APPLICANT: Leshkowitz, Dena
APPLICANT: Kita, David
APPLICANT: Kita, David
APPLICANT: Garcia, Veronica
APPLICANT: Garcia, Veronica
APPLICANT: Garcia, Veronica
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Birgit
TITLE OF INVENTION: HUMAN GENES AND GENE EXPRESSION PRODUCTS
TITLE OF INVENTION: HUMAN GENES AND GENE EXPRESSION
FILE REFERENCE: 2300-16252
CURRENT APPLICATION NUMBER: US/10/012,697
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: 60/254,648
PRIOR APPLICATION NUMBER: 60/254,668
PRIOR APPLICATION NUMBER: 60/275,668
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 1568
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.1%; Score 88.8; DB 17; Length 812; 78.9%; Pred. No. 4e-15; tive 1; Mismatches 33; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature

LOCATION: 734, 811

COTHER INFORMATION: n = A,T,C or G

US-10-012-697-1343
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LOCATION: 734, 811
OTHER INFORMATION: n = A,T,C
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LOCATION: 734, 811
OTHER INFORMATION: n = A,T,C
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NAME/KEY: misc_feature
LOCATION: 734, 811
OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: n = A, T, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 78.9
Matches 142; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: 734, 811
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| GARBEAL INFORMATION:
| APPLICANT: Endege, Wilson
| APPLICANT: Endege, Wilson
| APPLICANT: Endege, Wilson
| APPLICANT: Endege, Wilson
| APPLICANT: Monahan, John
| TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
| TITLE OF INVENTION: HUMAN PROSTATE CANCER
| TITLE OF INVENTION: HUMBER: 09/10/357,930
| CURRENT APPLICATION NUMBER: 06/183,319
| PRIOR PELING DATE: 2003-02-04
| PRIOR PELING DATE: 2000-02-17
| PRIOR PELING DATE: 2000-03-16
| PRIOR PELING DATE: 2000-06-09
| PRIOR PILING DATE: 2000-01-18
| PRIOR PILING DATE: 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        420 AGGCAGCAGATAATGGCAGCTNTAAACTCCCAGACTGCCGTGCAGTTCCCAGCAGTATGC 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           539 AAGÇAGCAGATAATGGCAGCTTTAAACTCGCAGACTGCCGTGCAATT-CCAGCAGTATGC 597
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                                                                   6.3%; Score 91.8; DB 20; Length 535; 92.2%; Pred. No. 4e-16; Live 0; Mismatches 8; Indels 1
                                                                                                                                                                                                                                                         Sequence 55215, Application US/10357930 Publication No. US20040259086A1 GENERAL INFORMATION:
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APPLICANT: Garcia, Pablo Dominguez
APPLICANT: Garcia, Altaf
APPLICANT: Scott, Beth
APPLICANT: Scott, Beth
APPLICANT: Crkvenjakov, Radoje
APPLICANT: Drmanac, Radoje
APPLICANT: Drmanac, Radoje
APPLICANT: Drmanac, Snezana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1343, Application US/10012697
Publication No. US20030215803A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: n = A, T, C or G
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Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Jones, Lee William
APPLICANT: Stache-Crain, Birgit
TITLE OF INVENTION: HUMAN GENES AND GENE EXPRESSION PRODUCTS
TITLE OF INVENTION: ISOLATED FROM HUMAN PROSTATE
FILE REFERENCE: 2300-16252
CURRENT APPLICATION NUMBER: US/10/012,697
                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 171; Indels
                                                                                                                                                                                                                                                                                                                                                                Score 78.4; DB 17;
Pred. No. 3.6e-12;
             PRIOR FILING DATE: 2000-08-14
PRIOR PLING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: US 60/148,934
PRIOR PLING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: US 60/148,933
PRIOR FILING DATE: 1999-08-12
PRIOR PLING DATE: 2000-01-18
PRIOR PLING DATE: 2000-01-18
PRIOR PLING DATE: 2000-01-18
PRIOR PLING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 69
SEQ ID NO 13
APPLICATION NUMBER: US/09/639,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1045, Application US/10012697
Publication No. US20030215803A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Escobedo, Jaime
APPLICANT: Garcia, Pablo Dominguez
APPLICANT: Kassam, Altaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lamson, George
Scott, Beth
Drmanac, Radoje
Crkvenjakov, Radomir
Dickson, Mark
                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Synthetic DNA
                                                                                                                                                                                                                                                                                                                                                                  5.4%;
                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Labat, Ivan
Leshkowitz, Dena
Kita, David
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 51.44
Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-012-697-1045/c
                                                                                                                                                                                                                                                                                                                            US-10-465-217-13
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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US-10-029-386-22859

Sequence 22859, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Pank, David R.

APPLICANT: Hanzel, David R.

TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     836 ACTGAAAATTCCGAAAAAGTCCTTGAGCCAGAAGCTGCAGAAGAAGAAGCCTTGGAAAATGGA 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     587 ACTGACAGCTCCGAAAACGAACTGGAACCAGAAGCTGCAGAAGAAGAGCCCTGGAGAATGGA 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            776 AAGGTGAACACAGCTGGAGCAAGTGATACACTGTCAGTTAATGGACAGGCCAAAACCCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 19, 529, 630, 630, 660, 669, 681
LOCATION: 656, 658, 659, 660, 669, 681
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: misc_feature
; LOCATION: 19, 592, 630, 634, 635, 639, 648, 649, 650, 651, 653, 655,
; LOCATION: 656, 658, 659, 660, 669, 681
; OTHER INFORMATION: n = A,T,C or G
US-10-012-697-1045
                                                                                                                                                                                                                                                                                                                                         648, 649, 650, 651, 653, 655,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               655,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33; Indels
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CURRENT FILING DATE: 2001-12-20
CURRENT FILING DATE: 2001-12-20
SOFTWARE: Annomax Sequence Listing Engine vers: 1:1
SEQ ID NO 22859
LENGTH: 628
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 77.2; DB 17;
Pred. No. 9.9e-12;
0; Mismatches 33;
PRIOR APPLICATION NUMBER: 60/254,648
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 60/275,668
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 1568
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: 19, 592, 630, 634, 635, 639,
LOCATION: 656, 658, 659, 660, 669, 681
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 19, 592, 639, 634, 635, 639,
LOCATION: 656, 658, 659, 660, 669, 681
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: 19, 592, 630, 634, 635, 639,
LOCATION: 656, 658, 659, 660, 669, 681
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 74.0%;
Matches 94; Conservative
                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                    SEQ ID NO 1045
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Sequence 1, Application US/09894273

Sequence 1, Application US/09894273

Publication No. US20040037847A1

GENERAL INFORMATION:

APPLICANT: Kaff, Elliott D.

APPLICANT: Kaye, Kenneth M.

TITLE OF INVENTION: VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO ITILE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE

TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE

CURRENT APPLICATION NUMBER: US/09/894,273

CURRENT APPLICATION NUMBER: US 60/109,422

PRIOR FILING DATE: 1998-11-19

NUMBER OF SEQ ID NOS: 3

SEQ ID NO 1

SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGÉTGTGCCCGGAGGAGGTCAAGACTCCACTGCCCTGAAGCAAACAAGGC 512
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                                                                                                                                                                                                                                                                               Length 628;
                                   OTHER INFORMATION: MAP TO ACO11553.3

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.8

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.0

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.96

OTHER INFORMATION: SWISSPROT HIT: P02461, EVALUE 3.60+00

OTHER INFORMATION: NT HIT: AJ277881.1, EVALUE 2.40e+00

OTHER INFORMATION: EST_HUMAN HIT: BF891619.1, EVALUE 7.00e-54
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                                                                                                                                                                                                                                                                             5.1%; Score 74.2; DB 16;
47.3%; Pred. No. 7.3e-11;
tive 0; Mismatches 248;
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; ORGANISM: Kaposi's sarcoma-associated herpesvirus
VS-09-894-273-1
                                                                                                                                                                                                                                                                                                   Best Local Similarity 47.3
Matches 223; Conservative
ORGANISM: Homo sapiens
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US-09-894-273-1
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                                                                      TGAGACGGGAGGAGGAGGAGGCGGCGGATAGAGGAAGAGAGGCTTCGGCTGGAACAGC
                                                                                                                                           Gaps
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   Length 3489;
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                                    Indels
 Score 74.2; DB 11;
Pred. No. 2e-10;
0; Mismatches 228;
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   5.1%;
Query Match
Best Local Similarity 50.3
Matches 236; Conservative
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